

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 12351

TO: Christopher Yaen

Location: REM/3A20/3C18

Art Unit: 1642 June <u>4</u>, 2004

Case Serial Number: 09/700770

From: P. Sheppard

Location: Remsen Building

Phone: (571) 272-2529

sheppard@uspto.gov

Search Notes	

STIC-Biotech/ChemLib

From:

Yaen, Christopher

Sent:

Wednesday, June 02, 2004 10:33 AM STIC-Biotech/ChemLib

To:

Subject:

09700770

could you please search seq id 7, 8, and 9

thanks

Chris

Christopher Yaen US Patent Office Art Unit 1642 571-272-0838 **REM 3A20 REM 3C18**

Searcher:
Phone:
Location:
Date Picked Up:
Date Completed:
Searcher Prep/Review:
Clerical:
Online time:

TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

VENDOR/COST (where a	pplic.)
STN:	
DIALOG:	
Questel/Orbit:	
DRLink:	
Lexis/Nexis:	
Sequence Sys.:	
WWW/Internet:	
Other (specify):	

Q89xu3 bradyrhizob Q8rpts corynebacte Q89h46 bradyrhizob Q8c313 mus musculu Q910k1 streptomyce Q86d11 leishmania Q9hni9 halobacteri

Q9yeg2 aeropyrum p O8xrm8 ralstonia s bifidobacte

Q8nq28 corynabacte Q8ej01 shewarella Q9dub5 galleria me Q9dub5 galleria me Q9d25m1 streptomyce Q9i5i2 pseudomonas Q9i5i2 pseudomonas Q9yar5 caulobacter Q9w137 bordetella Q7w7q0 bordetella Q7w7q0 bordetella Q7w7q0 bordetella Q7w7q0 bordetella Q74cv5 gamma-prote Q94cv5 gamma-prote Q97ywc1 toxoplasma Q88kel pseudomonas

093i77 thermus the Q9bhf9 leishmania Q7w2m5 bordetella

75 99

4;

Score

Result No. Perfect score:

Sequence:

1

OM protein

Run on:

Scoring table:

Total number Minimum DB Maximum DB

Database

Searched:

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N [1] —
REQUENCE FROM N.A.
RA MEDINE=22326074; PubMed=12438750;
RA Mini T., Copeland N.G., Gilbert D.J., Jenkins N.A., Srisodsai A.,
RA Zimonjic D.B., Kack-Waggoner C.L., Popescu N.C., Kimura S.;
RI "Cloning, expression, and chromosomal localization of the mouse gene
RT (Scgb3al, alias Ugrp2) that encodes a member of the novel uteroglobin-
RT related protein gene family.;
RL Cytogenet. Genome Res. 97:120-127(2002).
RL GMBL, AR313457; AANG2328.1;
DR MGD, MGI:1915912; Scgb3al.

CRT Schill AR313457; AANG328.1;
CHRISTON MGD, MGI:1915912; Scgb3al.

CRT Schill AR313457; AANG328.1;
CRT SCHILL AR31457; AANG328.1;
CRT SCH
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
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Last sequence update)
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Q8C313
Q9LOK1
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Q8NQ28
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01-MAR-2003 (TrEMBLrel.
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Q82ln6 streptomyce
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     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Q82LN6

RESULT 2 Q82LN6

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STRAIN-YS-314 / AJ 12310 / DSM 44549 / JCM 11189;

Kawarabayasi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y., Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y., Usuda Y., Sugimoto S.;

"The entire genomic sequence of Corynebacterium efficiens YS-314.";

Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AP06515; BAC17109.1; -.

HYpotherical protein; Complete proteome.

SEGUENCE 281 AA; 28188 MW; 3143B69C35048C2D CRC64;
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EMBL, AL939108; CAB99157.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 247 AA; 22950 MW; EE32ABD76
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SC01277 OR 2SCG18.24.
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X MEDLINE=22608306; PubMed=12692562;

X MEDLINE=22608306; PubMed=12692562;

A Stakai, Y. Hardran J. Hanamoto A., Shinose M., Kikuchi H., Shiba T.,

Sakai, Y., Hattori M., Omura 8., Shinose M., Kikuchi H., Shiba T.,

"Complete genome sequence and comparative analysis of the industrial

microorganism Streptomyces avermithis.";

Nat. Biotechnol. 21:526-531(2003).

REMBL; ARO05029; Bacc66885.1;

RGO; GO:0006508; F:methionyl aminopeptidase activity; IEA.

GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

InterPro; IPR002467; Peptidase M24.

InterPro; IPR001714; Peptidase M24.

R InterPro; PR001714; Peptidase M24.

R Pfam; PP00557; Peptidase M24.

R Pfam; PR00557; Peptidase M24.

R Pfam; PR00557; Peptidase M24.

R Pfam; PR00557; Peptidase M24.

R Pfam; PR00559; RAPEPTIDASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165, MEDLINE=21477403; PubMed=11572948; Omura S., Ikeda H., Ishikawa U., Hanamoto A., Takahashi C., Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T., Kikuchi H., Shiba T., Sakaki Y., Hattori M., "Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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Aminopeptidase; Complete proteome.
SEQUENCE 255 AA; 26727 MW; 0C41CD3010F855A3 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                  Streptomycineae; Streptomycetaceae; Streptomycee.
                                                                                      255 AA
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01-0TN-2003 (TrEMBLrel. 24, Last seq
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NCBI_TaxID=152794; [1] SEQUENCE FROM N.A.

Q8FST3

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STRAIN=A3(2) / M145;
MEDLINE=21996410; PubMed=12000953;
MEDLINE=21996410; PubMed=12000953;
MEDLINE=21996410; PubMed=12000953;
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Hange C.-H., Kieser H., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murpby L., Oliver K., O'Neil S.,
Rabbinowiteoft E., Rajandream M.A., Rutherford K., Futter S.,
Marren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J., "Complete genome sequence of the model actinomycete Streptomyces 39; 23; 16.4%; Score 82.5; DB 16; Length 247; 31.8%; Pred. No. 8.3; tive 10; Mismatches 40; Indels 23. / Match 16.6%; Score 83.5; DB 16; Length 281; Iocal Similarity 30.1%; Pred. No. 7.7; nes 40; Conservative 9; Mismatches 45; Indels 39; Streptomyces coelicolor. Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; 60 LLSSL--GIPVNHLIEGSQKCVAELGPQAVGAVKALKALLGALTVFG 104 121 LTGAAGGGNPLAAALGGAGNPLAALG----GAANPLAAVGGAAGALG 163 EE32ABD76146881B CRC64; 01-OCT-2000 (TrEMBLrel. 15, Created) 01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Streptomycineae, Streptomycetaceae, Streptomyces à

DR GO; GO:0006810; P:transport; IEA. DR InterPro; IPR000515; BPD transp. DR Pfam; PF00528; BPD_transp; 2. KW Complete proteome. SQ SEQUENCE 601 AA; 61216 MW; 78601FC5AB2DCB9C CRC64;	Query Match 15.4%; Score 77.5; DB 16; Length 601; Bast Local Similarity 30.7%; Pred. No. 63; Matches 42; Conservative 10; Mismatches 48; Indels 37; Gans 4:	QY 3 LAALLGLCVALSCSSAAAFLVGSAKDVAQPVAALESAAEAGAG 45	
Putative membrane protein. BP1449. Bordetella pertussis. Bacteria, Proteobacteria; Betaproteobacteria, Burkholderiales; Alcaligenacae, Bordetella. NCBI_TaxID=520;	(1) SEQUENCE FROM N.A. STRAIN-TOhama I / ATCC BAA-589 / NCTC 13251;	MEDLINE=22827954; PubMed=12910271; Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N., Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L., Cerdeno-Tarraga A.M., Temple L., James K., Harris B., Ohail M.	Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I., Chillingworth T., Collins M., Cronin A., Davis P., Doggett J., Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K., Leather S. Moule S. Morberczak H., O'Neil S., Ormond D., Price C.,

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EA BU Arabidopsis sequencing project; RI Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases. RI SUDMITTED (JUN-1999) to the EMBL/GenBank/DDBJ databases. RA ROSE M., Hempel S., Entian KD., Mewes H.W., Lemcke K., Mayer K.F.X.; RI Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. RA SEQUENCE FROM N.A. RA BU Arabidopsis sequencing project; RU Arabidopsis sequencing project; RU Arabidopsis sequencing project; RU BENEL, ALO79344; CAR45328.1; DR EMBL, ALO79344; CAR45328.1; DR EMBL, ALO79344; CAR45328.1; DR GO; GO:0016787; F:huclectide diphosphatase activity; IEA. DR GO; GO:0016787; F:nuclectide metabolism; IEA. DR GO; GO:0016781; P:nuclectide metabolism; IEA. DR GO; GO:0009117; P:nuclectide metabolism; IEA. DR GO; GO:0009117; P:nuclectide metabolism; IEA. DR Hydrolase. SRQUENCE 496 AA; 54678 MW; BDC2B4346121D732 CRC64;	Query Match 16.1%; Score 81; DB 10; Length 496;	ID QBXW23 PRELIMINARY; PRT; 148 AA. AC QBXW23; DT O1-MAR-2002 (TrEMBLrel. 20, Created) DT O1-MAR-2002 (TrEMBLrel. 20, Last sequence update) DT O1-CGT-2003 (TrEMBLrel. 25, Last annotation update) DT O1-CGT-2003 (TrEMBLrel. 25, Last annotation update) DF Probable lipoprotein. GN RSC2652 OR RS04564. OS Ralstonia solanacearum (Pseudomonas solanacearum). C Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; OC Burkholderiaceae; Ralstonia. OX NCBI TaxID=305; RN [1] RR SEQUENCE FROM N.A. RC STRAIR=GMI1000;	
RESULT 5 998CR1 AC 098CR1 AC 098CR1 DT 0-CCT-2001 (TrEMBLrel. 18, Last sequence update) DT 0-CCT-2001 (TrEMBLrel. 18, Last sequence update) DT 0-CCT-2003 (TrEMBLrel. 25, Last annotation update) DT 0-CCT-2003 (TrEMBLrel. 25, Last annotation update) DT 0-CCT-2003 (TrEMBLrel. 26, Last annotation update) DT 0-CCT-2003 (T		SQ SEQUENCE 694 AA; 73126 MW; 19E4978531DCF6CC CRC64; SQ SEQUENCE 694 AA; 73126 MW; 19E4978531DCF6CC CRC64; Query Match Best Local Similarity 33.3%; Pred. No. 25; Matches 33; Conservative 11; Mismatches 42; Indels 13; Gaps 4; Matches 33; Conservative 11; Mismatches 42; Indels 13; Gaps 4; OY 3 LAALGCVALSCSAAAFLOWS-ARPVAQPVAALESAAEAGAGTIANPLGTINPL 57 Db 438 MVPLFGISEAMDAAGAAAFIGWAWAEDQAVQAVALKAL 96 OY 58 KLLLSSLGIPWHALIEGSGXCVAELGQAVGAVKALKAL 96 Db 490 KARLIKAGLPVPKGERAGNAVEAVISSMALGFPVALKAL 528	RESULT 6 Q9SUB3 ID Q9SUB3 PRELIMINARY; PRT; 496 AA. AC Q9SUB3; DT 01-MAY-2000 (TrEMBLrel. 13, Created) DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) DT Minlantida mirronhocharan.

Nat. Genet. 35:32-40(2003). EMBL. BK64645; CRE33127.1; Complete protecome. SEQJENCE 229 AA; 22750 MW; 5A04498C4875195F CRC64;	Query Match Best Local Similarity 32.0%; Pred. No. 22; Matches 32; Conservative 15; Mismatches 30; Indels 23; Gaps 4;	11 VALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLLLSSLGIPVNH 70	71 LIBGSQKCVAELGPQAVGAVKALKALIGALTVFG 104 : :: :	
SO NY BY E	QAZ	δγ Op	ζζ Qq	-
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) DE Putative invasion protein. S \$AV294. S Experomyces avermitilis.	OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; OC Streptomycineae; Streptomycetaceae; Streptomyces. OX NCBI_TaxID=33903; RN [1]	RP SEQUENCE FROM N.A. RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165; RX PRODINGE-21477403; PubMeda-11572948; RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,	RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T., RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.; RF "Genome sequence.of an industrial microorganism Streptomyces RT avermitilis: deducing the ability of producing secondary	The second state of the se

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Query Match 15.3%; Score 77; DB 17; Length 453; Best Local Similarity 27.8%; Pred. No. 52; No. 52; Matches 30; Conservative 20; Mismatches 34; Indels 24; Gaps 4; Qy 11 VALSCSSAAAFIVGSAKPVAQPALESBAAERGAGTLANPLGFLINPLKLLLSSLGI 66 Db 102 MAAKAGADVAILIGSAADD-STILDDALSBAHKYQVRVMADLISAPERIKRAVDLEALGYDY 160	SULT 14 SULT 14 OBUAL4; OBUAL4; OL-UNN-2002 (TERMELRE]. 21, Created) OL-UNN-2003 (TERMELRE]. 21, Last sequence update) OL-UNN-2003 (TERMELRE]. 21, Last sequence update) OL-UNN-2004 (TERMELRE]. 21, Last sequence update) OL-UNN-2005 (TERMELRE]. 22, Last annotation update) OL-UNN-2005 (TERMELRE]. 25, Last annotation update)	

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MEDLINE=21396515; PubMed=11481438;

Krop I.E., Sgroi D., Porter D.A., Lunetta K.L., LeVangie R., Seth I Kaelin C.M., Rhei E., Bosenberg M., Schnitt S., Marks J.R., Pagon I Belina D., Razumovic J., Polyak K.;

"HIN-1, a putative cytokine highly expressed in normal but not cancerous mammary epithelial cells.";

Proc. Natl. Acad. Sci. U.S.A. 98:9796-9801(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- FUNCTION: Potential growth inhibitory cytokine.
-!- SUBCELLULAR LOCATION: Secreted (By similarity).
-!- SIMILARITY: Belongs to the uteroglobin family. UGRP subfamily.
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Uteroglobin-related protein 2 precursor (Cytokine HIN-1) (High in normal-1) (Secretoglobin family 3A member 1).
SCGB3A1 OR UGRP2 OR HIN1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=21539178; PubMed=11682631;
Niimi T., Keck-Waggoner C.L., Popescu N.C., Zhou Y., Levitt R.C.,
                                                                                                         ..
                                                                    Length 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 104 UTEROGLOBIN-RELATED PROTEIN 2.
104 AA; 10591 MW; D62F0E601FB57A6D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49.8%; Score 250; DB 1; Length 104; 57.0%; Pred. No. 8.2e-16;
                                                                                                                                                                                                                                           61 LSSLGIPVNHLIEGSQKCVAELGPQAVGAVKALKALLGALTVFG 104
                                                                                                                                                                                                           61 LSSLGIPVNHLIEGSQKCVAELGPQAVGAVKALKALLGALTVFG 104
 UTEROGLOBIN-RELATED PROTEIN
                                                                                                       1; Indels
                  R -> A (IN REF. 2).
1083873C8FAE8015 CRC64;
                                                     Score 497; DB 1,
NO. 7.2e-38;
                                                                                     Pred. No. 7.2e
0; Mismatches
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(Rel. 41, Last seq
(Rel. 41, Last ann
                                   10185 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF313456; AAL26216.1; -.
                                                                                     Sest Local Similarity 99.0%;
Aatches 103; Conservative
                                                                      99.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:1915912; Scgb3a1
Cytokine; Signal.
                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
                                   104 AA;
                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
 21
                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2003
                                                                                                                                                                                                                                                                                                                                     UGR2 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kimura S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Si
Matches 61
              CONFLICT
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                                                                    Query Match
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 CHAIN
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1 MKL-AALLGLCVALSCSSAAAFLVGS-AKPVAQPVAALESAAEAGAGTLAN-PLGTLNPL 57

Gaps

9

26; Indels

14; Mismatches

Conservative

61;

à

Local Similarity

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MEDINE-22388257; PubMed=12477932;

XX BILINE-22388257; PubMed=12477932;

XI Stusher R.D., Colling F.S., Wargner L., Shenmen C.M., Schuler G.D.,

XI Stusher R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Halen B. F.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Halen E.,

A Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,

Stapleton M., Saares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millahy S.J.,

Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S.W., Morgwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

Rahards S.W., Muzny D.W., Sodergren B.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska M.A.;

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@i8b-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- SUBUNIT: Homodimer.
-!- SUBCELLUIAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Highly expressed in lung.
-!- TISSUE SPECIFICITY: Highly expressed in lung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21539178; PubMed=11682631;
Nimi T., Keck-Waggoner C.L., Popescu N.C., Zhou Y., Levitt R.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Uteroglobin-related protein 1 precursor (Secretoglobin family 3A
                                                                                                                                                            58 KLLLSSLGIPVNHLIEGSQKCVAELGPQAVGAVKALKALLGALTVFG 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                       A
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                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCGB3A2 OR UGRP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MIM, 606531; -. Signal.
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139
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                                                                                                                                                                                                                  Local Similarity
                                                                    82
                                                                                                          92
      107
                                                                                                                                                                                                                                      34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota;
      VAESPLIC
                                                                  VARSPLIC
                                                                                                            VARSPLIC
                                                                                                                                                      SEQUENCE
                                                                                                                                                                                          Query Match
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      SHEFFFF
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                                                                                                                                                                    1 MKLAALLGLCVALSCS-SAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKL 59
                                                                                                                                                                                                              1 MKLVTIFLLVTISLCSYSATAFLINKVPLPVDKLAPL------PLDNILPFMDPLKL 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "UGRP1, a uteroglobin/clara cell secretory protein-related protein, is a novel lung-enriched downstream target gene for the T/BBP/NKX2.1
                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=0920H1-3; Sequence=VSP 006726;
-!- TISSUE SPECIFICITY: Highly expressed in lung.
-!- SIMILARITY: Belongs to the uteroglobin family. UGRP subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Niimi I., Keck-Waggoner C.L., Popescu N.C., Zhou Y., Levitt R.C.,
                                                                                                                                                                                                                                                                                                                                                                                                      UGR1_MOUSE STANDARD; PRT; 139 AA.
Q920H1; Q920H2; Q920H3;
Q920H2; Q920H3; Created)
28-FRB-2003 (Rel. 41, Last sequence update)
28-FRB-2003 (Rel. 41, Last annotation update)
Uteroglobin-related protein 1 precursor (Secretoglobin family 3A
                                                                                                                                10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UTEROGLOBIN-RELATED PROTEIN 1.
POTENTIAL.
UTEROGLOBIN-RELATED PROTEIN 1.
                                                                               Score 160; DB 1; Length 93;
Pred. No. 8.1e-08;
9; Mismatches 38; Indels
                                                                                                                                                                                                                                                        60 LLSSLGIPVNHLIEGSOKCVAELGPOAVGAVKALKALLGAL 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isold=Q920H1-2; Sequence=VSP_006727, VSP_06728;
                                                                                                                                                                                                                                                                                   FBD4BFAC2BF33718 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORMS A; B AND C).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=Q920H1-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF274960; AAL25709.1; -.
EMBL; AF274961; AAL25710.1; -.
MGD; MG1.2153470; Scgb3a2.
G0; G0:0005576; C:extracellular; IDA.
G0; G0:0005516; F:protein binding; IPI.
InterPro; IPR006038; Uteroglobin_supf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   homeodomain transcription factor.";
Mol. Endocrinol. 15:2021-2036 (2001).
-!- SUBUNIT: Homodimer.
-!- SUBCELLULAR LOCATION: Secreted.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Lung;
MEDLINE=21539178; PubMed=11682631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF274959; AAL25708.1; -.
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  1 21
22 93
93 AA; 10161 MW;
                                                                                    31.9%;
                                                                                                        43.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF01099; Uteroglobin;
                                                                                                                              Conservative
                                                                                    Query Match
Best Local Similarity
                                                                                                                            44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kimura S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=C
                                                                                                                                                                                                                                                                                                52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    member 2)
                                          SEQUENCE
  SIGNAL
                                                                                                                              Matches
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1 MKLAALLGLCVALSCSSAAAFIVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLL 60
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CATALYTIC ACTIVITY:

nicotinamide + {ADP-D-ribosyl} (N+1) -acceptor.

nicotinamide + {ADP-D-ribosyl} (N+1) -acceptor.

SUBUNIT: Oligomerizes and associates with TNK2. Interacts with the cytoplasmic domain of InPEP/Otame in SLC2A4/GLUT4-vesicles. Binds to the N-terminus of telomeric TRF1 via the ANK repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the telomeric PARP, tankyrase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21602874; PubMed=11739745;
Cock B.D., Dynek J.N., Chang W., Shostak G., Smith S.;
"Role for the related poly(ADP-Ribose) polymerases tankyrase 1 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIINE=20556282; PubMed=10988299;
Chi N.-W., Lodish H.F.;
Tankyrase is a Golgi-associated mitogen-activated protein kinase
substrate that interacts with IRAP in GLUT4 vesicles.";
J. Biol. Chem. 275:38437-38444(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Testis;
MEDLINE=99040105; PubMed=9822378;
Smith S., Giriat I., Schmitt A., de Lange T.;
"Tankyrase, a poly(ADP-ribose) polymerase at human telomeres.";
Science 282:1484-1487(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- FUNCTION: May regulate vesicle trafficking and modulate the subcellular distribution of SLC2A4/GLUT4-Vesicles. Has PARP activity and can modify TRF1, and thereby contribute to the regulation of telomere length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Last sequence update)
10-CT-2003 (Rel. 42, Last annotation update)
Tankyrase 1 (EC 2.4.2.30) (TANK1) (Tankyrase 1) (TNKS-1) (TRF1-interacting ankyrin-related ADP-ribose polymerase).
TNKS OR TNKS1 OR TIN1 OR TINF1 OR PARPL.
VSVLFLPMICAYPRDSKKQTFAFIERVFEOSKL
HU (in isoform B).
/FTId=VSP 006726.
VIIICSY -> BALSHLV (in isoform A).
                                                                                                                                                                                                                                                                                                                                                           10;
                                                                                                                                                                                                                                                                                        DB 1; Length 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                           36; Indels
                                                                                          VIIICSY -> BALSHLV (in isof
/FIId=VSP 006727.
Missing (in isoform A).
/FIId=VSP 006728.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION, AND MUTAGENESIS OF HIS-1184 AND GLU-1291.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 LSSLGIPVNHLIEGSQKCVAELGPQAVGAVKALKALL 97
                                                                                                                                                                                                                                                                                        26.9%; Score 135; DB 1
35.1%; Pred. No. 2e-05;
tive 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Smith S., de Lange T.;
"Cell cycle dependent localization of the te.
to nuclear pore complexes and centrosomes.";
J. Cell Sci. 112:3649-3656(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1327 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION.
MEDLINE=99454782; PubMed=10523501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         at human telomereв.";
Mol. Cell. Biol. 22:332-342(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            095271; 095272;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last seq
                                                                                                                                                                                                                            139 AA; 15431 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION, AND PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                           Conservative
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The Buropean Bicinformatics Institute.

The Buropean Bicinformatics Institute of the same of the statement is not as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensee@ibb.sib.ch).
SUBCELLULAR LOCATION: Cytoplasmic, associated with the Golgi and with juxtanuclear SLC2A4/GUTV4-vesicles. A minor proportion is also found at nuclear pore complexes and around the pericentriclar matrix of mitotic centromeres. During interphase, a small fraction of TMXS is found in the nucleus, associated with TRF1.

EVENT. SLEENALIVE PRODUCTS:

EVENT. SLEENALIVE PRODUCTS:
                                                                                                                                                                                                                                                                                    IsoId=095271-2; Sequence=VSP 004538, VSP 004539;
Note=No experimental confirmation available;
TISSUE SPECIFICITY: Ubiquitous; highest levels in testis.
PTM: Upon insulin-stimulation, phosphorylated on serine residues by MAPK kinases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MH, 603303; -.
GO; GO:000781; C:chromosome, telomeric region; IDA.
GO; GO:0003950; F:NAD ADP-ribosyltransferase activity; IDA.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0007004; P:telomerase-dependent telomere maintenance; NAS.
InterPro; IPR002110; ANK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transferase; Glycosyltransferase; NAD; Golgi stack; Telomere;
                                                                                                                                                                                                                                                                                                                                                                                                                         -1- PTM: ADP-ribosylated (-auto).
-1- SIMILARITY: Belongs to the PARP family.
-1- SIMILARITY: Contains 15 ANK repeats.
-1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nuclear protein; Repeat; ANK repeat; ADP-ribosylation;
Phosphorylation; Alternative splicing.
                                                                                                                                                                                                                                 IsoId=095271-1; Sequence=Displayed;
Name=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POLY-PRO.
POLY-SER.
POLY-SER.
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PROSITE; PS50297; ANK REP REGION; 1.
PROSITE; PS50105; SAM DOMAIN; 1.
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ANK 11.

ANK 112.

ANK 113.

ANK 115.
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EMBL, AF082557; AAC79842.1; --
EMBL, AF082558; AAC79843.1; --
EMBL, AF082559; AAC79844.1; --
HSSP, QO0420; AAC7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00023; ank; 19.
Pfam; PF00536; SAM; 1.
PRINTS; PR01415; ANKYRIN.
SMART; SM00248; ANK; 17.
SMART; SM00454; SAM; 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 313
4433
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556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      69
                                                                                                                                                                                                                                                                                                                                                                                                                 CSSAAAFLVGSAKPVAQPVAALESAA----EAGAGTLANPLGTLNPLKLLLSSLGIPVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Nature 417:141-147(2002).
-!-CATALYTIC ACTIVITY: Anthranilate + phosphoribosyldiphosphate = N-5'-phosphoribosyl-anthranilate + diphospharibosyl-anthranilate + diphospharibosyl-anthranilate + SIMILARITY: Belongs to the anthranilate phosphoribosyltransferase
                                                                                                                                                                                                                                                                                                                                                          Gaps
EST -> GHS (in isoform 2).

#Trid=VPD 004538.

#Ind=VSP 004539.

/FTId=VSP 004539.

/FTId=VSP 004539.

/FTId=VSP 004539.

/FTId=VSP 004539.

/FTIG=VSP 004539.

/FTIG=VSP 004539.

/FTIG=VSP 07 ACTIVITY; WHEN ASSOCIATED CONTROL OF ACTIVITY OF ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=A3(2) / M145,
MEDLINE=A1996410; PubMed=12000953;
MEDLINE=A1996410; PubMed=12000953;
MEDLINE=A1996410; PubMed=12000953;
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Horsbyr T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                             16.5%; Score 83; DB 1; Length 1327; 30.5%; Pred. No. 6.5; tive 13; Mismatches 43; Indels
                                                                                                                                                                                                          WITH A-1184.
MW; E14DE985C710B957 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Anthranilate phosphoribosyltransferase 2 (BC 2.4.2.18)
TRPD2 OR SCO3212 OR SCE8.05C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomycineae, Streptomycetaceae, Streptomyces.
NCBI_TaxID=1902;
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HAMAP: MF_00211; -; 1.

InterPro; IPR0005940; Ant_phapho_trans.

InterPro; IPR000312; Glyco_trans_3.

Pfam; PF02885; Glycos_trans_3N; I.

Pfam; PF00591; Glycos_trans_3N; I.
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                                                             1327
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         643
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29;
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      VARSPLIC
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                                                                VARSPLIC
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ID TRD2_ST
AC Q9Z4W9;
                                                                                                                       MUTAGEN
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MDC1 HUMAN
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                                                                                                                                                   117 LGVRIDLGABEAAACLDRIGITFLFAPVFHP--AFRHTAGPRRELGARTVFNLLGPLCNP 174
                                                                                                                              26
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIATURE-98101471; PubMed=9440521;
Bayle D., Waengler S., Weitzenegger T., Steinhilber W., Volz J.,
Bayle D., Waengler K.P., Sachs G., Melchers K.,
Przybylski M., Schaefer K.P., Sachs G., Melchers K.,
"Przybriki M., Schaefer K.P., Sachs G., Melchers K.,
"Properties of the P-type Appease encoded by the copAP operons of
Helicobacter pylori and Helicobacter felis.";
J. Bacteriol. 180:317-329(1998).
-! - FUNCTION: PROBABLY INVOLVED IN COPPER EXPORT.
-! - CATALYTIC ACTIVITY: ATP + H(2)O + Cu(2+)(In) = ADP + phosphate +
Cu(2+)(Out).
-! - SUBCELLULAR LOCATION: Integral membrane protein.
-! - SIMILARITY: Belongs to the cation transport Afpases family (P-type
ATPASES). Subfamily IB.
-! - SIMILARITY: Contains 1 HMA domain.
                                                                                                                              7 LGLCVALSCSSAAAFLVGSA----KPVAQPVAALESAA----EAGAGTLANPLGTL-NP
                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
NCBI_TaxID=214;
                                                                                                    12;
                                                                         15.3%; Score 77; DB 1; Length 335; llarity 34.5%; Pred. No. 6.5; Conservative 9; Mismatches 36; Indels
                TIGREAMS; TIGRO1245; trpD; 1.—
Tryptophan biosynthesis; Transferase; Glycosyltransferase;
Complete proteome.
SEQUENCE 335 AA; 34536 MW; 2706194E400B2F0D CRC64;
                                                                                                                                                                                                                                                                                                15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Copper-transporting ATPase (EC 3.6.3.4)
                                                                                                                                                                                                                                                                        732 AA
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175 SGARLRTLGVPSRELVEPMTEVLERLG 201
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Pfam; PF00122; E1-E2 ATPase; 1.
Pfam; PF00403; HNA; 1.
Pfam; PF00702; Hydrolase; 1.
PRINTS; PR00119; CATATPASE.
PRINTS; PR00943; CUATPASE.
TIGREAMS; TIGR01511; ATPASE.
                                                                                                                                                                                 57 LKLLLSSLGIPVNHLIEGSQKCVAELG 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR006403; ATPase-IB1 Cu.
InterPro; IPR006416; ATPase-IB hvy.
InterPro; IPR001757; ATPase E1-E2.
InterPro; IPR001756; Cu.ATPase.
InterPro; IPR008250; E1-E2 ATPase reg.
InterPro; IPR006121; HeavyMe_transpt.
InterPro; IPR005834; Hydrolase.
     PD001864; Glyco_trans_3; 1.
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PIR; T47269; T47269.
                                                                                                                                                                                                                                                                         STANDARD;
                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                  Helicobacter felis.
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=ATCC 49179;
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447 LLTLCASLEAQSEHVIAKGIVAHAKEQGIALOEVQEVQAKPGFGIKGVVGDQIIKAGNLE
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TIGREAMS; TIGRO1525; ATPase-IB hvy; 1.
TIGREPAMS; TIGRO1494; ATPase_P-type; 3.
PROSITE; BRO0154; ATPASE_E1_B2; 1.
PROSITE; PSO1047; HMA_1; 1.
PROSITE; PSSO846; HMA_2; 1.
Transport; Ion transport; Copper transport; Hydrolase; ATP-binding;
Machal-binding; Copper; Magnesium; Transmembrane; Phosphorylation.
1 88 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Buteleostomi;
Catarrhini; Hominidae; Homo.
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MEDLINE=21145589; PubMed=11247670;
MEDLINE=21145589; PubMed=11247670;
Wines M.E., Lee L., Katari M.S., Zhang L., DeRossi C., Shi Y.,
Wines M.E., Lee L., Katari M.S., Zhang L., Holdener B.C.;
Perkins S., Feldman M., McCombie W.R., Holdener B.C.;
"Identification of mesoderm development (mesd) candidate genes ladentification of mesoderm development (mesd) candidate genes comparative mapping and genome sequence analysis.";
Genomics 72:88-98(2001).
-- SIMILARITY: SOME, TO TALIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHOSPHORYLATION (BY SIMILARITY) COPPER (POTENTIAL).
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Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17; Mismatches 39; Indels
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MAGNESIUM (BY SIMILARITY).
7105107EA5949EFD CRC64;
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Mesoderm development candidate 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        362
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Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        613 M
78853 MW;
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Matches 35; Conservative
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359
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663
683
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732
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421
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16
609
613
732 AA;
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83

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RA MEDLINE=22388257; PubMed=12477932;

RA Klausner R.D., Collins P.S., Wagner L., Shemmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B.B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Ride S., Garcia A.M., Gay L.J., Hulyk S.W.,

R. Richards S., Worley K.C., Ride S., Garcia A.M., Gay L.J., Hulyk S.W.,

R. Norligues S., Worley K.C., Ride S., Garcia A.M., Gay L.J., Hulyk S.W.,

R. Richards S., Worley K.C., Schmutz J., Myers R.M.,

R. Blakesley R.W., Touchman U.W., Green E.D., Dickson M.C.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

R. Generation and initial analysis of more than 15,000 full-length

R. Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).

C. -- SIMILARITY: SOME, TO TALIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 LVELGDLVVSLTECSAHAAYLAAVATPGAQPALVDRYRVTRCRHEVEQGCAVLRATP 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----VAALESAAEAGAGTL-ANP 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota, Metazoa; Chordata, Craniata; Vertebrata, Euteleostomi; Mammalia, Butheria, Rodentia, Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wines M.E., Lee L., Katari M.S., Zhang L., DeRossi C., Shi Y., Perkins S., Feldman M., McCombie W.R., Holdener B.C.; "Identification of mesoderm development (mesd) candidate genes by comparative mapping and genome sequence analysis."; Genomics 72:88-98(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                          Genew; HGNC:13519; MESDC1.
SEQUENCE 362 AA; 37758 MW; 37BF391D663E1D6E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33;
                                                                                                                                                                                                                                                                                                                                                                                                                           Match 14.9%; Score 75; DB 1; Local Similarity 35.4%; Pred. No. 11; les 28; Conservative 6; Mismatches 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 LAALLGLCVALS-CSSAAAFLVGSAKPVAQP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               362 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21145589; PubMed=11247670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mesoderm development candidate 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               172 LADMTPQLLLEVSQGLSRN 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LGTLNPLKTLLSSLGIPVN 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last seq
10-OCT-2003 (Rel. 42, Last anno
                                                                                                                                                                                                                                                                                        EMBL; AY007810; AAG41058.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=129/SvJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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           This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112 IVELGDLVVSLTECSAHAAYLAAVATPGAQPAQPGLVDRYRVTRCRHEVEQGCAVLRATP
                                                                                                                                                                                                                                                                       3 LAALLGLCVALS-CSSAAAFLVGSAKPVAQP------VAALESAAEAGAGTL-ANP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
16-207-2001 (Rel. 40, Last sequence update)
15-8AR-2004 (Rel. 43, Last annotation update)
Probable serine/threonine protein kinase SNFILK (EC 2.7.1.-) (HRT-20)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND REVISIONS TO 8; 16-18; 44-45; 316 AND 435.
                                                                                                                                                                                                                                              12;
                                                                                                                                                                                                             Length 362;
                                                                                                                                                                                                                                              Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ruiz J.C.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                               362 AA; 37786 MW; EFE9BBFC09BB7CB5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-435 FROM N.A., AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                              33;
                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                               Score 75; DB 1; Pred. No. 11; 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          779 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            subfamily.
-!- SIMILARITY: Contains 1 UBA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P24941; 1AQ1.
MGD; MGI:104754; SMf11k.
Interpro; IPR000719; Prot kinase.
Interpro; IPR008271; Ser thr pkin AS.
Interpro; IPR002290; Ser_thr pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Embryo;
MEDLINE=95200798; PubMed=7893599;
                                                                                                                                                                                                                                                                                                                                                                             172 LADMTPOLLLEVSOGLSRN 190
                                                                                                                                                                                                                                                                                                                                             LGTLNPLKLLLSSLGIPVN 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Myocardial SNF1-like kinase).
                                                                                                                                  EMBL; AF311213; AAG33620.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U11494; AAA67926.2; -.
                                                                                                                                                                                                                  14.9%;
35.4%;
                                                                                                                                                                                                                                 Local Similarion
nes 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                   MGD; MGI:1891420; Mesdc1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNIL MOUSE
Q60670;
                                                                                                                                                                                                                                                                                                                                               21
                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
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us-09-700-770-9.rsp

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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9R1US; Q9R081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       subfamily.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 CVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANP--LGTLNPLKLLLSSLGIP 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            atoms 2 and 3 of pyruvate and glyceraldehyde 3-phosphate to yield 1-deoxy-D-xylulose-5-phosphate (DXP) (By similarity).
-!- CATALYTIC ACTIVITY: Pyruvate + D-glyceraldehyde 3-phosphate = 1-deoxy-D-xylulose 5-phosphate + CO(2).
-!- COFACTOR: Binds 1 thiamine pyrophosphate per subunit (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; first step. -!- PATHWAY: Biosynthetic pathway to thiamine and pyridoxol; first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: Belongs to the transketolase family. DXPS subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        flies, Migglesworthia glossinidia.";
Nat. Genet. 32:402-407(2002)
-1- FUNCTION: Catalyzes the acyloin condensation reaction between C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=22297718; PubMed=12219091;
Akman L., Yamashita A., Watanabe H., Oshima K., Shiba T., Hattori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wigglesworthia glossinidia brevipalpis.
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Wigglesworthia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genome sequence of the endocellular obligate symbiont of tsetse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
InterPro; IPR001245; Tyr pkinase.

InterPro; IPR000449; UBA_domain.

Pfani PR00069; pkinase; 1.

PROJOM; PR00109; TYRKINASE.

S GMARK; SMO2020; S TKC; 1.

R PROSITE; PS00101; PROTEIN KINASE ATP; 1.

R PROSITE; PS00101; PROTEIN KINASE_DOM; 1.

R PROSITE; PS00108; PROTEIN KINASE_ST; 1.

R PROSITE; PS500109; PROTEIN KINASE_ST; 1.

R PROSITE; PS500109; PROTEIN KINASE_ST; 1.

R PROSITE; PS50030; UBA; 1.

R Transferase; Setine/threonine-protein kinase; ATP-binding.

DOMAIN 27 278 PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                14.7%; Score 74; DB 1; Length 779; 32.9%; Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
11-deoxy-D-xylulose 5-phosphate synthase (BC 2.2.1.7) (1-deoxy-D-xylulose-5-phosphate synthase) (DXP synthase) (DXP synthase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                      7B08131BC46D9C4E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             30;
                                                                                                                                                                                                                                                                                                  ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             11; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----GSQSATPVLQTQA 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 VNHLIEGSOKCVAELGPOA 86
                                                                                                                                                                                                                                                                                                                                                                      85027 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                       41
56
149
                                                                                                                                                                                                                                                                                                                                                                      779 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=36870;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DXS WIGBR
Q8D357;
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                                                                                                                                                                                                                                                                                                                                                 ACT SITE
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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BINDING
                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
DXS_WIGBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 IVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLLLSSLGIPVNHLIEGSQKCV-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Feldman J.D., Vician L., Crispino M., Hoe W., Baudry M.,
Herschman H.R.;
"The Kidz gene encodes a protein kinase induced by depolarization in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Probable serine/threonine protein kinase SNF1LK (BC 2.7.1.-) (Salt-inducible protein kinase)
SNF1LK OR SIK OR KID2.
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MEDLINE=99330184; PubMed=10403390;
MEDLINE=99330184; PubMed=10403390;
MEDLINE=99330184; PubMed=10403390;
MEDLINE=99330184; PubMed=10403390;
MEDLINE=99330184; PubMed=1040;
MEDLINE=99330184; MEDLINE=90404; MEDLINE=9040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transferame, Flavoprotein, Thiamine pyrophosphate,
Isoprene biosynthesis, Thiamine biosynthesis, Complete proteome.
SEQJENCE 626 AA, 69851 MW, C77008D2D82ABE21 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGRFAMS; TIGR00204; dxs; 1.—
PROSITE; PS00801; TRANSKETOLASE 1; 1.
PROSITE; PS00802; TRANSKETOLASE 2; FALSE NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.6%; Score 73.5; DE 30.0%; Pred. No. 24; Live 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    776 AA.
                                            HAWAP, MF 00315; -; 1.
InterPro; IPR00547; Dxs synth.
InterPro; IPR00547; Transketo C like.
InterPro; IPR005476; Transketolase C.
InterPro; IPR005475; Transketolase CR.
InterPro; IPR005474; Transketolase CR.
Fint, PP02779; transket pyr; 1.
Pfam; PP02779; transket pyr; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: Contains 1 UBA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 ELGPQAVGAVKALKALLGAL 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              606 SLGLDSIGIKEKIKNWLNFL 625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEBS Lett. 453:135-139(1999)
BAC24290.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Variation Acids Res. 25:2737-2744 (1997).

-!- CATALYTIC ACTIVITY: ATP + L-alanine + tRNA(Ala) = AMP +

-!- CATALYTIC ACTIVITY: ATP + L-alanyl-tRNA(Ala).

-!- CATALYTIC ACTIVITY: Cytoplasmic.

-!- SUBCELLULAR LOCATION: Cytoplasmic.

-!- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=HBB / ATCC 27634;
MEDLINE=9735144; PubMed=9207019;
Lechler A., Martin A., Zuleeg T., Limmer S., Kreutzer R.;
Lechler A., active 53 kDa fragment of overproduced alanyl-tRNA synthetase from Thermus thermophilus HBB specifically interacts with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
1-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Alanyl-tRNA synthetase (EC 6.11.7) (Alanine--tRNA ligase) (AlaRS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

14.6%; Score 73.5; DB 1; Length 776;
Best Local Similarity 33.7%; Pred. No. 28;
Matches 28; Conservative 11; Mismatches 31; Indels 1.
                                                                                                                                                                                                                                                                                                                                                    Transferase; Serine/threonine-protein kinase; ATP-binding DOMAIN 27 278 PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
R -> K (IN REF. 2).
7BF745AF28F17E6E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                               UBA.
ATP (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP (BY SIMILARITY)
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                  InterPro; IPR000719; Prot kinase.
InterPro; IPR000719; Ser thr pkin AS.
InterPro; IPR000271; Ser thr pkinase.
InterPro; IPR000290; Ser-thr pkinase.
InterPro; IPR000449; UBA_domain.
Pfam; PF00069; pkinase; I.
Proom; PD000001; Prot kinase; I.
PROSITE; PS0010; PROTEIN KINASE_ATP; I.
PROSITE; PS00109; PROTEIN KINASE_DOM; I.
PROSITE; PS00108; PROTEIN KINASE_DOM; I.
PROSITE; PS00108; UBA; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       546 -----GSQSATPVĽQSQAGLGA 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 VNHLIEGSQKCVAELGPQA-VGA 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HAMAP; MF 00036; -; 1.
InterPro; IPR003156; DHHA1.
InterPro; IPR002318; tRNA-synt_2c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84908 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                               343
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303
33
56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYA THETH P74941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACT SITE CONFLICT
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NP BIND
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                          6 LIGICVALSCSSAAAFIVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLLLSSLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDILINE-2160851; PubMed=11743194; Miller N., Blanchard M., MEDILINE-2160851; PubMed=11743194; Miller N., Blanchard M., Goddmer B., Hinkle G., Gattung S., Miller N., Blanchard M., Goddman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Cielo C., Slater S.; "Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58."; Science 294:2323-2328(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nester E.W.;
"The genome of the natural genetic engineer Agrobacterium tumefaciens
            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIINE=21608550; PubMed=11743193;
Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
Chen Y., Paulsen I.T., Eisen J.A., Ruppe D.D., Bovee D. Sr.,
Chapman P., Clendenning J., Deathbrage G., Gillet W., Grant C.,
Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.
Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY: ATP + succinate + CoA = ADP + succinyl-CoA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        similarity). Selongs to the succinate/malate CoA ligase beta
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                                                                                                                                                                 Length 882;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-78B-2003 (Rel. 41, Created)
28-78B-2003 (Rel. 41, Last sequence update)
28-78B-2003 (Rel. 42, Last annotation update)
50coinyl-CoA synthetase beta chain (RC 6.2.1.5) (SCS-beta).
50CC OR ATUG38 OR AGC 4780.
Agrobacterium tumefaciens (strain CS8 / ATCC 33970).
Bacteria, Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium
NCBI_TaxID=176299;
                                                                                                                                                                                                          Indels
                                                                                                                                                                                                        12; Mismatches 47;
                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                             739 VGEAALEERLEKLLAEL-KEKEREVESLKARL 769
                                                                                                                                                                                                                                                                                                                         97
                                                                                                                                                                                                                                                                                                                                                                                                                                                               397 AA
                                                                                                                                                                   14.6%; Score 73.5; I 32.6%; Pred. No. 32;
                                                                                                                                                                                                                                                                                                                           66 IPVNHLIEGSQKCVAELGPQAVGAVKALKALL
IPR006193; tRNA synt Ala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 294:2317-2323(2001).
                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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                                                                                                                                                                                        Similarity
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                                                                                                                                                                           Local Si.
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                                                                                                                                                                     Query Match
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us-09-700-770-9.rsp

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Matcher
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the European Bioinformatics Institute. There are no restrictions on its mee by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                  18 AAAFLVGSAKPVAQPVAALE-SAAEAGAGTLANPLGTLNPLKLLLSSLGIPVNHLIEGSQ 76
                                                                                                                                                                                                                                                                                                                                                                                                              -----RGKG 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97014266; PubMed=8861101;
Kaestner K.H., Schuetz G., Monaghan A.P.;
"Expression of the winged helix genes fkh-4 and fkh-5 defines domains
in the central nervous system.";
Mech. Dev. 55:221-230(1996).
                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Six members of the mouse forkhead gene family are developmentally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Wakaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
MCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                    12;
                                                                                                                                                                                                                                                                                                                                                                                                              8 AKALLKGYGAPVAEGVALLKVEEAEAAAKQLPGPLYV---VKSQIHAGG
                                                                                                                                                                                                                                                                                                                       DB 1; Length 397;
                                                                                                                                                                                                                                                                                                                      Query Match
14.3%; Score 72; DB 1; Length 397;
Best Local Similarity 36.2%; Pred. No. 21;
Matches 29; Conservative 8; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGRFAMS; TIGRO1016; succoabeta; 1.
PROSITE; PS01217; SUCCINYL COA LIG 3; FALSE NEG.
Ligase; Tricarboxylic acid Cycle; Complete proteome.
SEQUENCE 397 AA; 41899 WW; 223CLA33825764F9F CRO64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kaestner K.H., Lee K.H., Schloendorff J., Hiemisch H.,
Monaghan A.P., Schuetz G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOY-2000 (Rel. 39, Last annotation update)
Forkhead box protein B2 (Transcription factor FKH-4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                 HAMAP, MF 00558; -; 1.
InterPro, IPR003135; ATP-grasp.
InterPro; IPR005809; CoA lig_beta.
InterPro; IPR005811; CoA_ligase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=129;
MEDLINE=93361500; PubMed=7689224;
                                                                                                                                                                                                                                                                                                                                                                                                                                             96
                                                                                                                                                                                                                                                                                                                                                                                                                                                              K-FKELGPDAKGGVRLAKSI 76
                                                                                       EMBL, AE009211; AAL43619.1; -. EMBL, AE00817; AK88359.1; -. PIR, AE2900, AE2900. PIR; F97675;
                                                                                                                                                                                                                                                                                                                                                                                                                                           77 KCVAELGPQAVGAVKALKAL
                                                                                                                                                                                                             Pfam; PF02222; ATP-grasp; 1.
Pfam; PF00549; ligase-CoA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 4-114 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    regulated.";
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ID FXB2_MOUSE
AC Q64733;
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11 VALSCSSAAAFLVGSAKPVAQ-PVAALESAAEAGAGTLANPLGTLNPL-----KL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20;
                                                                                   RASP, 063445; 2HFH.

REANSPAC; T02442.

RWCD; WGI:1347468; Foxb2.

RWCD; WGI:1347468; Foxb2.

R InterPro; IPR001766; TF Fork head.

R FRINTS; PR00250; Fork head; 1.

R Probom; PR000425; TF Fork head; 1.

R PROSTITE; PR00657; FORK HEAD.; 1.

R PROSTITE; PS00658; FORK HEAD.; 1.

R PROSTITE; PS00058; FORK HEAD.; 1.

R PROSTITE; PS00099; FORK HEAD.; 1.

R PAGITE; PS00099; FORK HEAD.; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB8A8EFD1E94AB10 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29.2%; Pred. No. 28;
tive 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.1%; Score 71;
or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                               FORK-HEAD.
POLY-HIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             POLY-HIS.
POLY-PRO.
POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POLY-ALA.
POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45170 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 29.2%
nem 33; Conservative
                                          EMBL; X92591; CAA63335.1;
EMBL; X71942; CAA50744.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               428 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMEIN
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Search completed: June 2, 2004, 20:19:36 Job time : 5.04538 secs

59

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein

June 2, 2004, 20:14:10; Search time 7.07942 Seconds (without alignments) 1413.099 Million cell updates/sec Run on:

502 1 MKLAALLGLCVALSCSSAAA......QAVGAVKALKALLGALTVFG 104 US-09-700-770-9 Title: Perfect score: Sequence:

BLOSUM62 Scoring table: 283366 seqs, 96191526 residues Searched:

Gapop 10.0 , Gapext 0.5

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

pirl:* pir2:* pir3:* PIR 78:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	Description	probable phosphodi	hypothetical prote	probable transport		hypothetical prote		thio-disulfide int	copper-transportin	hypothetical prote	Д	probable aldehyde	gamma-glutamyltran	hypothetical prote	amastigote-specifi		Buccinyl-CoA synth	hypothetical prote	L-serine dehydrata	ATP-dependent Clp	endopeptidase clp	probable MFS trans	heat shock protein	probable endopepti		zinc finger protei		hypothetical prote	ical	probable PPE prote
SUMMARIES	ID	וסו	S60004	T35054	T36304	AD2973	G98309	H87275	T47269	H72647	C84358	F83553	B87315	T13613	A56010	AE2900	F97675	D70968	B87634	AC3070	F98216	CB3368	G85160	D71409	C86178	T46147	D82179	875653	G75454	C70582
	DB	เล			N																									7
		496	1381	601	335	355	355	669	732	544	331	502	584	1279	236	397	397	528	462	874	887	440	668	831	431	452	477	244	396	423
•	Query Match	16.1	15.8	15.4	15.3	15.1	15.1	15.1	15.1	15.0	14.6	14.5	14.5	14.5	14.3	14.3	14.3	14.3	14.2	4.	14.2	4.	4.	14.0	13.9	•	13.9	٠	•	13.8
	Score	i l	79.5	77.5	77	92	76	16	16	75.5	73.5	73	73	73	72	72	72	72	71.5	71.5	71.5	71	70.5	70.5	70	7.0	70	69.5	69.5	ė.
	Result No.	1	2	m	4	S	9	7	60	o,	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

probable L-serine hypothetical prote	Berine processusse, probable ATP-depen probable adhesin Y	hypothetical prote ferric enterobacti	ferric enterobacti ferric enterobacti	ferric enterobacti hypothetical prote branched-chain ami	hypothetical prote probable conserved similar to transla
AD0782 AF3312	D75393 T36551 AE0074	F84336 AB0575	116343 816296 A85558	E90707 F70719 C75312	H82706 B87247 B96671
000	200	000	7 77 79	0 0 0	000
170	627 853 3295	335	334 334 334	334 560 387	1179 1206 2698
13.8	13.7 13.7 13.7	13.6	13.5 13.5	13.5 13.5	13.4 13.4 13.4
69.5	0 0 0 0 0 0	68 8.5 7.0	68 68 68	68 68 67.5	67.5 67.5 67.5
30	9 9 9 9 8 8	3 9 8	3 3 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	0 4 4 0 1 2	4 4 4 6 4 5

ALIGNMENTS

T.		probable phosphodiesterase I (EC 3.1.4.1) / nucleotide diphosphatase (EC 3.6.1.9) Tl	C;Species: Arabidopsis thaliana (mouse-ear cress)	C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Aug-2002	Bion: T09931	R;Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Bancroft, I.; Mewes, H.W.; Mayer, K	submitted to the Protein Sequence Database, June 1999	A; Reference number: Z16897
RESULT 1	T09931	probable phospho	C;Species: Arabi	C, Date: 16-Jul-1	C, Accession: T09931	R;Bevan, M.; Ros	submitted to the	A;Reference numb

A; Molecule type: DNA
A; Medidus: 1-496 <BEV.
A; Residues: 1-496 <BEV.
A; Cross-references: EMBL:AL079344; GSPDB:GN00062; ATSP:T16L4.190
A; Experimental source: cultivar Columbia; BAC clone T16L4
C; Genetics:
A; Genetics: ATSP:T16L4.190
A; Map position: 4
C; Superfamily: human phosphodiesterase I / nucleotide pyrophosphatase C; Keywords: coenzyme A; metalloprotein; phosphoric diester hydrolase

Gaps 9 Query Match
16.1%; Score 81; DB 2; Length 496;
Best Local Similarity 41.3%; Pred. No. 5.2;
Matches 26; Conservative 14; Mismatches 17; Indels

3;

62 6 LLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGA--GTLANPLGTLN-PLKLLLS ଧ 셤

63 SLG 65 à g

114 SDG 116

hypothetical protein - common roundworm retrotransposon R4 (fragment)

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probable ABC transporter permease protein MJ0087 AGR_L_2865 [imported] - Agrobacteria probable ABC transporter permease protein MJ0087 AGR_L_2865 [imported] - Agrobacteria C;Species: Agrobacterium tumefaciens C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002 C;Accession: G9890: B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Gold A; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, Science 294, 2323-2328, 2001 A;A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium A;Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                               C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C;Accession: AD2973
R;Wood, D:W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McC; Karp, P.; Romero, P.; Zhang, S.
R;Karp, P.; Romero, P.; Zhang, S.
A;Ruthors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kal
                                                                                                                                                                                                                                                                                                                                       hypothetical protein Atu3389 [imported] - Agrobacterium tumefaciens (strain C58, Dup
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ster, E.W.
A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Reference number: AB2577; MUID:21608550; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: GB: AE007870; PIDN: AAK90001.1; PID: g15159970; GSPDB: GN00170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 SSLGIPVNHL-----IEGSQKCVA-----ELGPQAVGAVKALKALLGALTVF 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-355 «KUR»
A;Cross-references: GB:AE008689; PIDN:AAL44202.1; PID:g17741781; GSPDB:GN00187
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 SSLGIPVNHL-----IEGSQKCVA-----ELGPQAVGAVKALKALJGALTVF 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : :|: : | | | : | : | 74 WDIRMPIALMAVIVGASLSVAGAQMQTILSNPLASPFTLGISAAASFGAALALVGGVAIF 133
117 LGVRIDLGABEAAACLDRTGITFLFAPVFHP--AFRHTAGPRRELGARTVFNLLGPLCNP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 KLAALLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLLL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 RILILVGLFLALCFSMAADWALGPARYTLSEVLA-----TIADPAAVGNQLRVVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 KLAALLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 RILIINGLFLALCFSWAADMALGPARYTLSEVLA------TIADPAAVGNQLRVVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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11;
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Best Local Similarity 23.3%; Pred. No. 11;
Matches 28; Conservative 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22; Mismatches
                                                                                                                                                          175 SGARLRILGVPSRELVEPMTEVLERLG 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 76;
Pred. No.
                                                                              57 LKLLLSSLGIPVNHLIEGSQKCVAELG 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: AGR L 2865
A,Map position: linear chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Gene: Atu3389
A,Map position: linear chromosome
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Best Local Similarity 23.3%;
Matches 28; Conservative 2
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-355 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: AD2973
A;Status: preliminary
A;Molecule type: DNA
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R;Saunders, D.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, March 1999
A;Reference number: Z21604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable transport system permease protein - Streptomyces coelicolor C;Species: Taboutate: Ob. Nov-1999 #sequence_revision O5-Nov-1999 #text_change O5-Nov-1999 C;Accession: T35054
A;Resequer, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, August 1998
A;Resequer commber: Z21566
A;Reservence number: Z21566
A;Residues: TPOI proliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-601 <SEE>
A;Cross-references: EMBL:AL031371; PIDN:CAA20556.1; GSPDB:GN00070; SCOEDB:SC4G2.19
A;Experimental source: strain A3(2)
C;Genetics:
A;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-335 <SAU>
A;Residues: 1-335 <SAU>
A;Cross-references: EMBL:AL035654; PIDN:CAB38583.1; GSPDB:GN00070; SCOEDB:SCE8.05c
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: trpD2; SCOEDB:SCE8.05c
C;Superfamily: anthranilate phosphoribosyltransferase; trpD homology
                                                                                          ä,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 IGLCVALSCSSAAAFLVGSA----KPVAQPVAALESAA----EAGAGTLANPLGTL-NP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---QPVAALESAAEAGAG-----
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                                                                                                                                                                                                                                            27 IAMPCSTNSFFERGTPEPHREPISGTDSSESLGMGTHRSPRLNDDEVINGPKGHESDPVH
                                                                                              Gaps
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                                                                                          27;
                                                                                                                                                                     ---LANPLG-
               Length 1381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 601;
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15.3%; Score 77; DB 2; Length 335;
Best Local Similarity 34.5%; Pred. No. 8.2;
Matches 30; Conservative 9; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                          Indels
   48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.4%; Score 77.5; DB 2; 30.7%; Pred. No. 13; iive 10; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: T36304
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                 11 VALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGT
                                                                                                                                                                                                                                                                                                                                                                       3 LAALLGLCVALSCSSAAAFLVGSA--KPVA---
                                                                                                                                                                                                                                                                                                                           53 -----TLNPLKLLLSSLGIPVNHLIEGSQ 76
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Best Local Similarity 30.7%
Matches 42; Conservative
                                                                                                  Conservative
                       Query Match
Best Local Similarity
Matches 25; Conserv
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C;Accession: C84358
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, J. Letthauser, B.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, J. Letthauser, B.; Keller, K.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Js. Droc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; A;Reference number: A84160; MUID:20504483; PMID:11016950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero A; Reference number: A72450; MUID:99310339; PMID:10382966 A; Accession: H72647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Cross-references: DDBJ:AP000060, NID:g5104188; PIDN:BAA79584.1; PID:d1043370; PID:g
A,Experimental source: strain K1
                                                                                                                                                                                                                                                                                                                                                                     C.Species: Aeropyrum pernix
C.Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C.Accession: H7264;
E.Kawarahayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.;
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Vamazaki,
DNA Res. 6, 83-101, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'n
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   507 FFNLPNPFGTLEGIQVFVGTETQILGVVVLADSLKEGSKEAISEL--KALGVKTTLLSGD 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71
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C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 ALVAVAVAVAVAAALMSVGGRTAGLIAGAGEAASQSIAAASNPLYMEAWVEAGA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                      hypothetical protein APE0614 - Aeropyrum pernix (strain K1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 ALLGLCVALSCSSA-----AAFLVGSAKPVAQPVAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 75.5; DB
; Pred. No. 18;
19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.6%; Score 73.5; DE ilarity 27.9%; Pred. No. 17; Conservative 17; Mismatches
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26.4%;
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Best Local Similarity 26.4%
Matchem 33; Conservative
                                                                                                                                               577
                                                                             ----VKALKALLG 98
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565 NLENVRALATQLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1-544 <KAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100 LTVFG 104
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                                                                             90
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Best Local S
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                                                                      ò
                                                                                                                                                                                                              thio-disulfide interchange protein, probable [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 2.O.Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: H87275
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Bisen, J.; Heidelberg, J.B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon J., Ermolaeva, M.; White, O.; Salzata, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-414, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Status: preliminary
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Copper-transporting ATPase (EC 3.6.1.-) P-type copA [validated] - Helicobacter felis copper-transporting ATPase (EC 3.6.1.-) P-type copA [validated] - Helicobacter felis C;Species: Helicobacter felis C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 08-Sep-2000 C;Accession: T47269

E;Bayle, D.; Wangler, S.; Weitzenegger, T.; Steinhilber, W.; Volz, J.; Przybylski, M.; Sacteriol. 180, 317-329, 1998

A;Title: Properties of the P-type ATPases encoded by the copAP operons of Helicobacter A;Reference number: Z24437; MUID:98101471; PMID:9440521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:AE005673; NID:g13421344; PIDN:AAK22204.1; GSPDB:GN00148 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         545 VSMILGLLAVVGALALAAASALSAKP---PVAAAEASTPSGPGLTAE---AWSPEKVQAL 598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 15.1%; Score 76; DB 2; Length 699, Best Local Similarity 30.5%; Pred. No. 21; Matches 32; Conservative 18; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 SSLGIPVNHLIEGS-----QKCVAELGPQAVGAVKALKALL 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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A;Status: translated from GB/EMBL/DDBJ
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Matches 35; Conserv
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Succinyl-CoA synthetase beta chain [imported] - Agrobacterium tumefaciens (strain CE C; Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C;Accession: AB2900
R;Wood, D:W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Wc erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amastigote-specific protein A2 precursor - Leishmania donovani infantum C; Species: Leishmania donovani A56010 R; Charest, H.; Matlashewski, G. Mol. Cell. Biol. 14, 2975-2984, 1994 A; Title: Developmental gene expression in Leishmania donovani: differential cloning A; Reference number: A56010 MUID: 94217695; PMID: 7545921 A; Accession: A56010 A; Status: preliminary A; Molecule type: mRNA A; Residues: 1-216 CMAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-1279 <PAP>
A;Cross-references: EMBL:AL022018; NID:e1273253; PID:e1426350; PIDN:CAA17685.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              213 SANPAAAPSAARFSSHYSAKNAQFLRKPKPSEGGGGSLSS---TVKPVADILESLGIVSG 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKLAALLGLCVALSCSSAAAFLVGSAKP--VAQPVAALESAAEAGAGTLANPLGTLNPLK 58
                                                                                      hypothetical protein 8D8.2 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C;Accession: T13613
R;Papagiannakis, G.; Spanos, L.; Cox, S.; Siden-Kiamos, I.; Louis, C.
submitted to the EMBL Data Library, April 1999
A;Description: Sequencing the distal X chromosome of Drosophila melanogaster.
A;Reference number: Z17695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 SAKPVAQPVAALESA-----AEAGAGTLANPLGTLNPLKLLLSSLGIPVN 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKIRSVRPLVVLLVCVAAVLALSASAEPHKAAVDVGPL-SVGPQSVGPLSVGPQAVGPLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.5%; Score 73; DB 2; Length 1279; 31.6%; Pred. No. 75; ive 12; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 LLLSSLGIPVNHLIEGSOKCVAELGPQAVGAVKALKALLGALTV 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:S69693; NID:g546453; PID:g546454
C;Superfamily: proline-rich protein
C;Keywords: tandem repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70 HLIEGSQK-----CVAELGPQ-AVGAVKALKALLGA 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.3%; Score 72; DB 2; 29.8%; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: FlyBase:FBgn0024367
A;Introns: 65/2
A;Note: EG:8D8.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 31.69
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: T13613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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AE2900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ద
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ਨੇ
                                                                                                                                                                                                                         probable aldehyde dehydrogenase PA0747 [imported] - Pseudomonas aeruginosa (strain PAO1) C;Species: Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa C;Accession: F83553 A;Accession: F83554 A;Accessi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gamma-glutamyltransferase [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C;Accession: B87315
B; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Nelson, K.E.; Eisen, J.; Haft, D.H.; Kolon, N.J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: B87315
A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      264 AQVLGNLVGASCGAAGQRCMAISAAVFVGAAREWIPELAERMAVLRPGHWQDPDAAYGPL 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 KLAALLGLCVALSCSSAAAFLVGSAKPVAQPV--AALESAAEAGAGTLANPLGTINPLKL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---AAFLVGSAK----PVAQPVAALESA----AEAGAGTL 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: PA0747
C;Superfamily: aldehyde dehydrogenase (NAD+); aldehyde dehydrogenase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 502;
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---IPVNHLIEGSQKCVAELGPQAVGAVKALKALLGAL 100
                                         38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41; Indels
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28.6%; Pred. No. 34;
iive 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.5%; Score 73; DB 29.1%; Pred. No. 29; iive 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Residues: 1-584 <STO>
A,Cross-references: GB:AE005673; NID:gl34
C,Genetics
C,Gene: CC0531
C,Superfamily: gamma-glutamyltransferase
                                                        137 VLGSERVTPFPLNFLFRG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 28.6%
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63
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Matches
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Query Match
Best Local Similarity 36.2%; Pred. No. 28;
Matches 29; Conservative 8; Mismatches 31; Indels

Gaps

18 AAAFLVGSAKPVAQPVAALE-SAAEAGAGTLANPLGTLNPLKLLLSSLGIPVNHLIEGSQ 76

Op à g

77 KCVAELGPOAVGAVKALKAL 96

58 K-FKELGPDAKGGVRLAKSI 76

Search completed: June 2, 2004, 20:22:23 Job time: 9.07942 secs

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June 2, 2004, 20:19:10; Search time 18:5413 Seconds (without alignments) 1578.054 Million cell updates/sec
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502
1 MKLAALLGLCVALSCSSAAA......QAVGAVKALKALLGALTVFG 104
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1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/USIOA_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1155919 segs, 281338677 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                           - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES		
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Result	a room	Query	Query Match Length DB	H.C.	T.	Description	
	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		1111111111111	1			
н	502	100.0	104	σ	US-09-989-722-408	Seguence 408, App	
7	502	100.0		6	US-09-989-723-408	Sequence 408, App	
m	502	100.0		σ	US-09-989-279-408	Sequence 408, App	
4	502	100.0		σ	US-09-989-727-408	Sequence 408, App	
Ŋ	502	100.0		თ	US-09-989-731-408	Sequence 408, App	
٥	502	100.0	104	Q	US-09-989-732-408	Sequence 408, App	
7	502	100.0		0	US-09-991-073-408	Sequence 408, App	
80	502	100.0		σ	US-09-990-442-408	Sequence 408, App	
σ	502	100.0		6	US-09-991-163-408	Sequence 408, App	
10	502	100.0		σ	US-09-993-604-408	Sequence 408, App	
11	502	100.0		σ	US-09-990-456-408	Sequence 408, App	
12	502	100.0		0	US-09-989-721-408	Sequence 408, App	
13	502	100.0		6	US-09-992-598-408		
14	502	100.0		σ	US-09-989-293A-408	Sequence 408, App	
15	502	100.0	104	σ	US-09-989-735-408	Sequence 408, App	

App	App	App	App	App	App	App	App	App	App	App	App	App	App	App	App	App	App	App	App	App	App	App	App	App	App	App	App	App	App
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Sequence				Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Seguence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
US-09-990-444-408	-09-991-181-40	-989-730-40	-436-40	US-09-993-687-408	9-989-73	-09-997	9-66-60-	-997	-997	US-09-990-438-408	-990-562-4	-990	189-726-4	-156-	437-4	-157	514	19-997	-60	06-60	19-997	109-260-601	066-60	-854-4	US-09-997-628-408	09-997-683-40	09-989-729A-4	-09-997-3	US-09-997-440-408
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ALIGNMENTS

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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same File REFRENCE: P2730F1C63
CURRENT APPLICATION NUMBER: US/09/989,722
CURRENT FILING DATE: 2001-11-19
Sequence 408, Application US/0999722
Patent No. US20020072067A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
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PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
                                                                                                                                                                                                                                                                             Grimaldi, J. Christopher
Gurney, Austin L.
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Williams, P. Mickey
Wood, William I.
Zhang, Zemin
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                                                                                                                                         Eaton, Dan L.
Ferrara, Napoleone
Fong, Sherman
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Roy, Margaret Ann
                                                                                                                                                                                                                    Gerritsen, Mary E.
Goddard, Audrey
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                                                                                Baker, Kevin P.
Botstein, David
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                                                                                                                         Desnoyers, Luc
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NUMBER: 60/065186 1997-11-12 NUMBER: 60/065311 1997-11-13 NUMBER: 60/06770 1997-11-24 NUMBER: 60/075945 1998-02-25 NUMBER: 60/078910 1998-03-26 NUMBER: 60/078910 1998-03-26 NUMBER: 60/078910 1998-03-26 NUMBER: 60/078910 1998-03-26 NUMBER: 60/08910 1998-03-26 NUMBER: 60/084600	NUMBER: 60/087106 1998-05-28 1098-06-02 NUMBER: 60/087605 NUMBER: 60/087605 NUMBER: 60/08755 1998-06-02 1998-06-03 1998-06-03 1998-06-04 NUMBER: 60/088025 1998-06-04 NUMBER: 60/088021 1998-06-04 NUMBER: 60/08803 1998-06-04 NUMBER: 60/08803 1998-06-04 NUMBER: 60/08803 1998-06-04 1998-06-04 NUMBER: 60/08803 1998-06-04 NUMBER: 60/08803 1998-06-04 NUMBER: 60/08803 1998-06-04 NUMBER: 60/08803 1998-06-06 NUMBER: 60/08803 1998-06-06 1998-06-06 NUMBER: 60/08803 1998-06-06 1998-06-06 1998-06-06	NUMBER: 60/08855 1998-06-09 1998-06-10 1998-06-10 NUMBER: 60/088738 1998-06-10 NUMBER: 60/08810 1998-06-10 NUMBER: 60/08824 1998-06-10 NUMBER: 60/08824 1998-06-10 NUMBER: 60/08828 1998-06-10 NUMBER: 60/08858 1998-06-11 NUMBER: 60/08861 1998-06-11 NUMBER: 60/08861 1998-06-11 NUMBER: 60/08861 1998-06-11 NUMBER: 60/08861 1998-06-11 NUMBER: 60/08861 1998-06-11 NUMBER: 60/088976 1998-06-11 NUMBER: 60/088976 1998-06-11 NUMBER: 60/089105 11998-06-11 NUMBER: 60/089105 11998-06-11
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PRIOR APPLICATION NUMBER: 60/089514
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PRIOR APPLICATION NUMBER: 60/089538
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PRIOR PLING DATE: 1998-06-17
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PRIOR PLING DATE: 1998-06-25
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FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088655
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APPLICATION NUMBER: 60/089512
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FILING DATE: 1998-06-16
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APPLICATION WIMBER: 60/078910
APPLING DATE: 1998-03-20
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APPLICATION NUMBER: 60/087106
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FILING DATE: 1998-06-10
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APPLICATION NUMBER: 60/088858
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APPLICATION NUMBER: 60/089105
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FILING DATE: 1998-06-04
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APPLICATION NUMBER: 60/088030
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APPLICATION NUMBER: 60/088326
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FILING DATE: 1998-06-11
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                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/084600
FILING DATE: 1998-05-07
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APPLICATION NUMBER: 60/087607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/087609
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APPLICATION NUMBER: 60/087759
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APPLICATION NUMBER: 60/087827
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APPLICATION NUMBER: 60/088021
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; Pred. No. 7.5e-47;
0; Mismatches 0; Indels
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CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
                                                                                   OR FILING DATE: 1998-07-02

OR APPLICATION NUMBER: 60/091514

OR APPLICATION NUMBER: 60/091544

OR APPLICATION NUMBER: 60/091519

OR FILING DATE: 1998-07-02

OR FILING DATE: 1998-07-02

OR APPLICATION NUMBER: 60/091626

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OR APPLICATION NUMBER: 60/091633

OR FILING DATE: 1998-07-02

OR APPLICATION NUMBER: 60/091978

OR PILING DATE: 1998-07-07

OR APPLICATION NUMBER: 60/091982

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Patent No. US20020072092A1
GENERAL INFORMATION:
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Grimaldi, J.Christopher
Gurney, Austin L.
Kljavin, Ivar J.
Napier, Mary A.
          AFFLILMS DATE: 1998-07-01
PILING DATE: 1998-07-01
TITING DATE: 1998-07-02
APPLICATION NUMBER: 60/091360
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
Tumas, Daniel
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Gerritsen, Mary E.
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Matches 104; Conservative
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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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AFFLACEMENT CARRELLY ACTIONS SECRETED and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730PLC6 CURRINT APPLICATION NUMBER: US/09/989,279
CURRINT APPLICATION NUMBER: US/00/9787
PRIOR APPLICATION NUMBER: 60/06250
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-11-12
PRIOR PLING DATE: 1997-11-12
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; Pred. No. 7.5e-47;
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          PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR PELING DATE: 1998-07-01
PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR APPLICATION NUMBER: 60/091633
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-07
PRIOR PELING DATE: 1998-07-07
PRIOR PELING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
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US-09-989-279-408
Sequence 408, Application US/09989279
Patent No. US20020072496A1
PATENT NO. USA02010N:
REPRICANT: Ashkenazi, Avi J.
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Gurney,Austin L.
Kljavin,Ivar J.
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Roy, Margaret Ann
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1998-07-02
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R APPLICATION NUMBER: 60/083322
RR FILING DATE: 1998-04-28
R PPLICATION NUMBER: 60/084600
R FILING DATE: 1998-05-07
R APPLICATION NUMBER: 60/087106
R FILING DATE: 1998-05-28
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FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088742
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APPLICATION NUMBER: 60/089598
FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/088858
FILING DATE: 1998-06-11
APPLICATION NUMBER: 60/08861
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APPLICATION NUMBER: 60/089105
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APPLICATION NUMBER: 60/089440
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APPLICATION NUMBER: 60/089514
FILING DATE: 1998-06-16
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FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/088826
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FILING DATE: 1998-06-02
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FILING DATE: 1998-06-03
PAPLICATION NUMBER: 60/088021
FILING DATE: 1998-06-04
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APPLICATION NUMBER: 60/088029
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APPLICATION NUMBER: 60/088030
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APPLICATION NUMBER: 60/088033
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APPLICATION NUMBER: 60/088167
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FILING DATE: 1998-06-05
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APPLICATION NUMBER: 60/088217
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TITILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C65
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100.0%; Pred. No. 7.5e-47;
iive 0; Mismatches 0;
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CURRENY FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 0(0.049787
PRIOR PELING DATE: 1997-06-16
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065319
PRIOR PILING DATE: 1997-11-24
PRIOR FILING DATE: 1997-11-24
PRIOR FILING DATE: 1998-02-25
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1938-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR PILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
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PRIOR FILING DATE: 1998-07-07
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Patent No. US20020072497A1
GENERAL INFORMATION:
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Grimaldi, J. Christopher
Gurney, Austin L.
Kljavin, Ivar J.
Napier, Mary A.
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Gerritsen, Mary E.
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Botstein, David
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Eaton, Dan L.
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US-09-989-727-408
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APPLICANT:
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60/088824

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PRIOR APPLICATION NUMBER: 60/09509
PRIOR FILING DATE: 1999 06-17
PRIOR PAPLICATION NUMBER: 60/09500
PRIOR FILING DATE: 1999 06-17
PRIOR FILING DATE: 1999 06-19
PRIOR PRIOR DATE: 1999 06-24
PRIOR PRIOR DATE: 1999 06-25
PRIOR PRIING DATE: 1999 06-25
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1 MKLAALLGLCVALSCSSAAAFIVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLL 60 Gaps ., 0 Length 104; 61 LSSLGIPVNHLIEGSQKCVAELGPQAVGAVKALKALLGALTVFG 104 61 LSSLGIPVNHLIEGSQKCVAELGPQAVGAVKALKALLGALTVFG 104 Indels ; Score 502; DB 9; ; Pred. No. 7.5e-47; 0; Mismatches 0; PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR PLICH DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/09182
PRIOR PILING DATE: 1998-07-07 Sequence 408, Application US/09989731 Patent No. US20020103125A1 GENERAL INFORMATION: APPLICANT: Ashkenazi,Avi J. Query Match
Best Local Similarity 100.0%;
Matches 104; Conservative 0 Ferrara, Napoleone FILING DATE: 1998-07-02 Botstein, David Desnoyers, Luc Eaton, Dan L. Fong, Sherman RESULT 5 US-09-989-731-408 셤 d ò

R APPLICATION NUMBER: 60/091519
R FILING DATE: 1998-07-02
R APPLICATION NUMBER: 60/091626
R FILING DATE: 1998-07-02
R APPLICATION NUMBER: 60/091633
R FILING DATE: 1998-07-02 R. FILING DATE: 1998-06-25
R. APPLICATION NUMBER: 60/090862
R. FILING DATE: 1998-06-26
R. APPLICATION NUMBER: 60/090863
R. APPLICATION NUMBER: 60/091360
R. APPLICATION NUMBER: 60/091360
R. APPLICATION NUMBER: 60/091478
R. APPLICATION NUMBER: 60/091478
R. APPLICATION NUMBER: 60/091478
R. APPLICATION DATE: 1998-07-01 R FILING DATE: 1998-06-25
R APPLICATION NUMBER: 60/090690
R FILING DATE: 1998-06-25
R APPLICATION NUMBER: 60/090694
R FILING DATE: 1998-06-25
R APPLICATION NUMBER: 60/090695
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R APPLICATION NUMBER: 60/090445
F FILING DATE: 1998-06-24
R FILING DATE: 1998-06-24
F FILING DATE: 1998-06-24
F APPLICATION NUMBER: 60/090535 APPLICATION NUMBER: 60/090542 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090557 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090676 APPLICATION NUMBER: 60/091544 FILING DATE: 1998-07-01 APPLICATION NUMBER: 60/090431 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090435 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090444 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090678 APPLICATION NUMBER: 60/090696 APPLICATION NUMBER: 60/090254 FILING DATE: 1998-06-22 APPLICATION NUMBER: 60/090349 APPLICATION NUMBER: 60/090540 APPLICATION NUMBER: 60/089653 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089801 FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089907
FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089908
FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089947 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/089948 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/089952 FILING DATE: 1988-06-19 APPLICATION NUMBER: 60/090246 FILING DATE: 1998-06-22 FILING DATE: 1998-06-23 APPLICATION NUMBER: 60/090355 FILING DATE: 1998-06-23 APPLICATION NUMBER: 60/090429 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090252 FILING DATE: 1998-06-24 FILING DATE: 1998-06-22 FILING DATE: 1998-06-24 1998-06-17 PRIOR | PRIOR PRIOR PRICR PRICR

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PRIOR FILING DATE: 1998-06-04

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PRIOR APPLICATION NUMBER: 60/089538

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PRIOR APPLICATION NUMBER: 60/089538

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PRIOR APPLICATION NUMBER: 60/089553

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PRIOR APPLICATION NUMBER: 60/089553

PRIOR PILING DATE: 19
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R APPLICATION NUMBER: 60/087827
R FILING DATE: 1998-06-03
R PILING DATE: 1998-06-04
R FILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/088025
                                                                             APPLICATION NUMBER: 60/087609
FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/087759
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FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088028
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APPLICATION NUMBER: 60/088029
FILING DATE: 1998-06-04
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APPLICATION NUMBER: 60/088033
FILING DATE: 1998-06-04
                      APPLICATION NUMBER: 60/087607
FILING DATE: 1998-06-02
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APPLICANT: Walliams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Zanay, Zemin.
ITILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPREMENT 2.70PLC27.
CURRENT APPLICATION NUMBER: US/09/989,732
CURRENT APPLICATION NUMBER: 60/06250
PRIOR APPLICATION NUMBER: 60/06250
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-11-12
PRIOR PLING DATE: 1997-11-12
PRIOR PLING DATE: 1997-11-13
PRIOR PLING DATE: 1997-11-13
PRIOR PLING DATE: 1998-02-25
PRIOR FILING DATE: 1998-02-25
PRIOR FILING DATE: 1998-03-05
PRIOR FILING DATE: 1998-05-07
PRIOR PLILING DATE: 1998-05-07
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100.0%; Score 502; DB 9;
Best Local Similarity 100.0%; Pred. No. 7.5e-47;
Matches 104; Conservative 0; Mismatches 0;
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PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
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Grimaldi, J.Christopher
Gurney, Austin L.
Kljavin, Ivar J.
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Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
Tumas, Daniel
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Eaton, Dan L.
Ferrara, Napoleone
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Paoni, Nicholas F.
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Gerritsen, Mary E.
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Botstein, David
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US-09-989-732-408
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PRIOR APPLICATION NUMBER: 60/08991
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-19
PRIOR FILING DATE: 1998-06-19
PRIOR FILING DATE: 1998-06-19
PRIOR PILING DATE: 1998-06-29
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PRIOR PILING DATE: 1998-06-20
PRIOR PILING DATE: 1998-06-20
PRIOR PILING DATE: 1998-06-23
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-25
PRIOR PILING DATE: 1998-06-25
PRIOR PILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/09065
PRIOR PILING DATE: 1998-06-25
PRIOR PILING DATE: 1998-06-26-29
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C15
                                                                                                                                                                  1 MKLAALLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLL
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100.0%; Score 502; DB 9;
Best Local Similarity 100.0%; Pred. No. 7.5e-47;
Matches 104; Conservative 0; Mismatches 0;
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PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-66-16
PRIOR APPLICATION NUMBER: 60/06250
PRIOR PILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-11-12
PRIOR PELING DATE: 1997-11-12
PRIOR PILING DATE: 1997-11-13
PRIOR PILING DATE: 1997-11-13
PRIOR PILING DATE: 1997-11-13
PRIOR PRIOR APPLICATION NUMBER: 60/065311
PRIOR PILING DATE: 1998-11-24
PRIOR FILING DATE: 1998-02-25
PRIOR PILING DATE: 1998-03-20
PRIOR PILING DATE: 1998-03-20
PRIOR PILING DATE: 1998-03-20
PRIOR PRIOR APPLICATION NUMBER: 60/083322
PRIOR PILING DATE: 1998-03-20
PRIOR PILING DATE: 1998-03-20
PRIOR PILING DATE: 1998-04-28
PRIOR PILING DATE: 1998-05-07
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APPLICATION NUMBER: 60/087106
FILING DATE: 1998-05-28
APPLICATION NUMBER: 60/087607
FILING DATE: 1998-06-02
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Patent No. US20020127576A1
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
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Gurney, Austin L.
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
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Williams, P. Mickey
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Gerritsen, Mary E.
Goddard, Audrey
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Napier, Mary A.
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Botstein, David
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GENERAL INFORMATION
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PRIOR FILING DATE: 1998-06-18

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PRIOR PRILATION NUMBER: 60/08947

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PRIOR PILING DATE: 1998-07-0

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OR APPLICATION NUMBER: 60/089532
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OR APPLICATION NUMBER: 60/089538
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R. PILING DATE: 1998-06-12
R. APPLICATION NUMBER: 60/089440
           R APPLICATION NUMBER: 60/087827

R FILING DATE: 1998-06-03

R APPLICATION NUMBER: 60/088021

R FILING DATE: 1998-06-04

R APPLICATION NUMBER: 60/088025

R FILING DATE: 1998-06-04

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R APPLICATION NUMBER: 60/088028

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APPLICATION NUMBER: 60/089907
FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089908
FILING DATE: 1998-06-18
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APPLICATION NUMBER: 60/089512
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APPLICATION NUMBER: 60/089653
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APPLICATION NUMBER: 60/088826
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APPLICATION NUMBER: 60/088858
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APPLICATION NUMBER: 60/088655
FILING DATE: 1998-06-09
APPLICATION NUMBER: 60/088734
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APPLICATION NUMBER: 60/088738
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APPLICATION NUMBER: 60/088742
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APPLICATION NUMBER: 60/088810
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FILING DATE: 1998-06-04
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APPLICATION NUMBER: 60/088326
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FILING DATE: 1998-06-05
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FILING DATE: 1998-06-05
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FILING DATE: 1998-06-05
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERENCE: P2730PLG
CURRENT APPLICATION NUMBER: US/09/990,442
REIGN APPLICATION NUMBER: US/04997
REIGN APPLICATION NUMBER: 60/04397
REIGN FILING DATE: 1997-10-17
REIGN APPLICATION NUMBER: 60/06231
REIGN APPLICATION NUMBER: 60/065311
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REIGN APPLICATION NUMBER: 60/065311
REIGN APPLICATION NUMBER: 60/065312
REIGN APPLICATION NUMBER: 60/065312
REIGN APPLICATION NUMBER: 60/06532
REIGN APPLICATION NUMBER: 60/06332
REIGN APPLICATION NUMBER: 60/08322
REIGN APPLICATION NUMBER: 60/087607
REIGN APPLICATION NUMBER: 60/087609
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                        100.0%; Score 502; DB 9;
100.0%; Pred. No. 7.5e-47;
iive 0; Mismatches 0;
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Patent No. US20020132252A1
GENERAL INFORMATION:
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Grimaldi, J.Christopher
Gurney, Austin L.
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
Tumas, Daniel
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Gerber, Hanspeter
Gerritsen, Mary E.
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                                                                         Matches 104; Conservative
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Botstein, David
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Eaton, Dan L.
                            Query Match
Best Local Similarity
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PRIOR APPLICATION NUMBER: 60/08994
PRIOR APPLICATION NUMBER: 60/08948
PRIOR APPLICATION NUMBER: 60/08952
PRIOR APPLICATION NUMBER: 60/09024
PRIOR APPLICATION NUMBER: 60/09025
PRIOR FILING DATE: 1998-06-22
PRIOR PILING DATE: 1998-06-22
PRIOR PILING DATE: 1998-06-23
PRIOR PILING DATE: 1998-06-24
PRIOR PELING DATE: 1998-06-25
PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-03
PRIOR PELING DATE: 1998-07-03
PRIOR PELING DATE: 1998-07-03
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Score 502; DB 9; Length 104; Pred. No. 7.5e-47;

100.0%; 100.0%;

Query Match Best Local Similarity

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APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PLC17
CURRENT APPLICATION NUMBER: US/09/991,163
CURRENT FILING DATE: 2001-11-14
MKLAALLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLL
                                                                                                           61 LSSLGIPVNHLIEGSQKCVAELGPQAVGAVKALKALLGALTVFG 104
                                                                                                                                              CURRENT FILING DATE: 2001-11-14

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR FILING DATE: 1997-10-17

PRIOR PELICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12

PRIOR PILING DATE: 1997-11-13

PRIOR FILING DATE: 1997-11-13

PRIOR FILING DATE: 1997-11-13

PRIOR FILING DATE: 1997-11-24

PRIOR FILING DATE: 1998-01-25

PRIOR PILING DATE: 1998-01-25

PRIOR PILING DATE: 1998-01-25

PRIOR PILING DATE: 1998-01-26

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PRIOR PILING DATE: 1998-01-28

PRIOR PELING DATE: 1998-01-28

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PRIOR PILING DATE: 1998-01-20

PRIOR PILING DATE: 1998-01-20

PRIOR PILING DATE: 1998-01-20
                                                                                                                                                                                                                                                                                                              Sequence 408, Application US/09991163
Patent No. US20020132253A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
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Kljavin, Ivar J.
Napier, Mary A.
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Eaton, Dan L.
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R FILING DATE: 1998-06-22 R APPLICATION NUMBER: 60/090252 R FILING DATE: 1998-06-22 A PPLICATION NUMBER: 60/090254 R FILING DATE: 1998-06-22 R APPLICATION NUMBER: 60/090349 FILING DATE: 1998-06-26
APPLICATION NUMBER: 60/090863
FILING DATE: 1998-06-26
APPLICATION NUMBER: 60/091360 APPLICATION NUMBER: 60/092182 FILING DATE: 1998-07-09 FILING DATE: 1998-07-01 APPLICATION NUMBER: 60/091478 APPLICATION NUMBER: 60/091544 FILING DATE: 1998-07-01 FILING DATE: 1998-07-01 APPLICATION NUMBER: 60/091519 FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091633 APPLICATION NUMBER: 60/091982 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090862 APPLICATION NUMBER: 60/091626 APPLICATION NUMBER: 60/091978 APPLICATION NUMBER: 60/090540 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090678 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090695 APPLICATION NUMBER: 60/090696 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090435 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090444 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090445 APPLICATION NUMBER: 60/090535 APPLICATION NUMBER: 60/090542 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090676 APPLICATION NUMBER: 60/090690 APPLICATION NUMBER: 60/090694 APPLICATION NUMBER: 60/090429 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090472 APPLICATION NUMBER: 60/090557 APPLICATION NUMBER: 60/090355 APPLICATION NUMBER: 60/090431 FILING DATE: 1998-07-02 1998-07-02 1998-07-07 ILING DATE: 1998-06-25 FILING DATE: 1998-06-25 FILING DATE: 1998-06-24 FILING DATE: 1998-06-25 FILING DATE: 1998-06-25 FILING DATE: 1998-06-24 'ILING DATE: 1998-06-24 FILING DATE: 1998-06-24 FILING DATE: 1998-06-23 1998-06-19 1998-06-19 LING DATE: 1998-06-23 FILING DATE: FILING DATE: FILING DATE: LING DATE: PRIOR ö

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RAPLICATION NUMBER: 60/089598
R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089599
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R FILING DATE: 1998-06-17
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FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/089952
FILING DATE: 1998-06-19
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APPLICATION NUMBER: 60/089532
FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089538
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APPLICATION NUMBER: 60/089801
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APPLICATION NUMBER: 60/089907
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APPLICATION NUMBER: 60/089908
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FILING DATE: 1998-06-19
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FILING DATE: 1998-06-16
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APPLICATION NUMBER: 60/088826
FILING DATE: 1998-06-10
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APPLICATION NUMBER: 60/088861
FILING DATE: 1998-06-11
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APPLICATION NUMBER: 60/089105
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APPLICATION NUMBER: 60/089514
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APPLICATION NUMBER: 60/088742
FILING DATE: 1998-06-10
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FILING DATE: 1998-06-10
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APPLICATION NUMBER: 60/088029
FILING DATE: 1998-06-04
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APPLICATION NUMBER: 60/088326
FILING DATE: 1998-06-04
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FILING DAFE: 1998-06-05
APPLICATION NUMBER: 60/088202
FILING DATE: 1998-06-05
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FILING DATE: 1998-06-05
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APPLICATION NUMBER: 60/088734
FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088738
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FILING DATE: 1998-06-04
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APPLICATION NUMBER: 60/088033
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C25
CURRENT APPLICATION NUMBER: US/09/993,604
CURRENT FILING DATE: 2001-11-17
                                                                                  61 LSSLGIPVNHLIEGSQKCVAELGPQAVGAVKALKALLGALTVFG 104
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PRIOR FILING DATE: 1997-06-16
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PRIOR FILING DATE: 1997-01-17
PRIOR FILING DATE: 1997-01-17
PRIOR FILING DATE: 1997-11-12
PRIOR PAPLICATION NUMBER: 60/065116
PRIOR FILING DATE: 1997-11-13
PRIOR PELING DATE: 1997-11-13
PRIOR PELING DATE: 1997-11-24
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PRIOR FILING DATE: 1998-03-20
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PRIOR PELING DATE: 1998-06-02
PRIOR PELING DATE: 1998-06-03
PRIOR FILING DATE: 1998-06-03
                                                                                                                                                                                                                                                                      Sequence 408, Application US/09993604 Patent No. US20020137075A1 GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
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Gurney,Austin L.
Kljavin,Ivar J.
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Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Roy, Margaret Ann
Stewart, Timothy A.
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Goddard, Audrey
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Gerber, Hanspeter
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Botstein, David
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Eaton, Dan L.
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US-09-993-604-408
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APPLICANY: Wood, Walliam 1.

APPLICANY: Wood, Walliam 1.

TITLIS OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLIS OF INVENTION: Acids Encoding the Same FILING PAPEL CATION NUMBER: US/09/90,456
CURRENT APPLICATION NUMBER: US/09/90,456
CURRENT FILING DATE: 1997-06-16
PRIOR PELING DATE: 1997-06-16
PRIOR PILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-12
PRIOR PELING DATE: 1997-11-13
PRIOR PELING DATE: 1998-11-13
PRIOR PELING DATE: 1998-10-26
PRIOR PELING DATE: 1998-05-06
PRIOR FILING DATE: 1998-05-07
PRIOR PELING DATE: 1998-06-07
LSSIGIPVNHLIEGSQKCVAELGPQAVGAVKALKALLGALTVFG 104
                                               LSSLGIPUNHLIEGSQKCVAELGPQAVGAVKALKALLGALTVFG 104
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R FILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/088025
R FILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/088026
R FILING DATE: 1998-06-04
                                                                                                                                                                                                               Sequence 408, Application US/09990456 Patent No. US20020137890A1 GENERAL INFORMATION:
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Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
Tumas, Daniel
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Eaton, Dan L.
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                      PRIOR APPLICATION NUMBER: 60/090252
PRIOR APPLICATION NUMBER: 60/090254
PRIOR PILLING DATE: 1998-06-22
PRIOR PELLING DATE: 1998-06-24
PRIOR FILLING DATE: 1998-06-24
PRIOR FILLING DATE: 1998-06-24
PRIOR PILLING DATE: 1998-06-24
PRIOR PELLING DATE: 1998-06-24
PRIOR PILLING DATE: 1998-06-25
PRIOR PILLING DATE: 1998-06-26
PRIOR PILLING DATE: 1998-07-02
PRIOR PILLING DATE: 1998-07-03
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Best Local Similarity 100.
Matches 104; Conservative
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PRIOR APPLICATION NUMBER: 60/08029
RRIOR FILING DATE: 1999-06-04
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RRIOR FILING DATE: 1998-06-04
RRIOR FILING DATE: 1998-06-07
RRIOR RELING DATE: 1998-06-10
RRIOR APPLICATION NUMBER: 60/08958
RRIOR RELING DATE: 1998-06-10
RRIOR APPLICATION NUMBER: 60/08959
RRIOR RELING DATE: 1998-06-17
RRIOR PELING DATE: 1998-06-17
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1 MKLAALLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLL 60 Gaps ö Length 104; 61 LSSLGIPVNHLIEGSQKCVAELGPQAVGAVKALKALLGALTVFG 104 LSSLGIPVNHLIEGSQKCVAELGPQAVGAVKALKALLGALTVFG 104 Indels ö 100.0%; Score 502; DB 9; 100.0%; Pred. No. 7.5e-47; Mismatches R FILING DATE: 1998-06-24
R APPLICATION NUMBER: 60/090435
R FILING DATE: 1998-06-24
R FILING DATE: 1998-06-24
R FILING DATE: 1998-06-24
R APPLICATION NUMBER: 60/090445 APPLICATION NUMBER: 60/091360 FILING DATE: 1998-07-01 APPLICATION NUMBER: 60/091478 FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091544 APPLICATION NUMBER: 60/092182 FILING DATE: 1998-07-09 APPLICATION NUMBER: 60/090472 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090535 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090540 APPLICATION NUMBER: 60/090862 FILING DATE: 1998-06-26 APPLICATION NUMBER: 60/090863 FILING DATE: 1998-06-26 APPLICATION NUMBER: 60/091519 FILING DATE: 1998-07-02 FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091633 FILING DATE: 1998-06-25
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FILING DATE: 1998-06-04

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A APPLICATION NUMBER: 60/089598
RILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089599
R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089600
R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089653
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R APPLICATION NUMBER: 60/08858
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R APPLICATION NUMBER: 60/088861
R FILING DATE: 1998-06-11
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R APPLICATION NUMBER: 60/088326

E FILING DATE: 1998-06-04

E APPLICATION NUMBER: 60/088167

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R APPLICATION NUMBER: 60/088202

R APPLICATION NUMBER: 60/088212
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APPLICATION NUMBER: 60/089908
FILING DATE: 1998-06-18
PAPLICATION NUMBER: 60/089947
FILING DATE: 1998-06-19
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FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/089952
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APPLICATION NUMBER: 60/090254
FILING DATE: 1998-06-22
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APPLICATION NUMBER: 60/089440
FILING DATE: 1998-06-16
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FILING DATE: 1998-06-16
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FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089538
FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/089801
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APPLICATION NUMBER: 60/088655
FILING DATE: 1998-06-09
APPLICATION NUMBER: 60/088734
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APPLICATION NUMBER: 60/088738
FILING DATE: 1998-06-10
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                           APPLICATION NUMBER: 60/088030
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088033
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APPLICATION NUMBER: 60/088217
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APPLICATION NUMBER: 60/
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CURRENT FILING DATE: 2001-11-19
PRIOR PELING DATE: 1997-06-16
PRIOR PELING DATE: 1997-06-16
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PRIOR PELING DATE: 1997-10-17
PRIOR PELING DATE: 1998-02-25
PRIOR PELING DATE: 1998-02-25
PRIOR PELING DATE: 1998-02-26
PRIOR PELING DATE: 1998-03-20
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APPLICATION NUMBER: 60/088028
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APPLICATION NUMBER: 60/088029
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US-09-989-721-408
; Sequence 408, Application US/09989721
; Patent No. US20020142961A1
; Patent No. US20020142961A1
; Patent No. HORNATION:
; APPLICANT: Ashkenazi, Avi J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Godowski, Paul J.
Grimaldi, J.Christopher
Gurney, Austin L.
Kljavin, Ivar J.
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Williams, P. Mickey
Wood, William I.
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Fong, Sherman
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Goddard, Audrey
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Botstein, David
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60/089907

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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acide Encoding the Same
FILE REFERENCE: P2730P1C20
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CURRENT PELING DATE: 2001-11-14

PRIOR PEPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR PELING DATE: 1997-10-17

PRIOR PELING DATE: 1997-11-12

PRIOR FILING DATE: 1997-11-13

PRIOR FILING DATE: 1997-11-24

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APPLICATION NUMBER: 60/088030
FILING DATE: 1998-06-04
                               408, Application US/09992598
5. US20020160384A1
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Gurney, Austin L.
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
Tumas, Daniel
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Paoni, Nicholas F.
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Goddard, Audrey
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Botstein, David
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PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR PELICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR PRILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/09069
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/09069
PRIOR FILING DATE: 1998-06-25
PRIOR PRILING DATE: 1998-06-25
PRIOR PILING DATE: 1998-06-26
PRIOR PILING DATE: 1998-06-26
PRIOR PILING DATE: 1998-06-26
PRIOR PILING DATE: 1998-07-01
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PRIOR FILING DATE: 1998-07-09
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Best Local Similarity 100.
Matches 104; Conservative
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R FILING DATE: 1998-06-17
R FILING DATE: 1998-06-17
R RELING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089599
R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089600
R FILING DATE: 1998-06-17
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R APPLICATION NUMBER: 60/088734
R FILING DATE: 1998-06-10
R FILING DATE: 1998-06-10
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088742
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R APPLICATION NUMBER: 60/088212
R FILING DATE: 1998-06-05
R FILING DATE: 1998-06-05
R FILING DATE: 1998-06-05
R APPLICATION NUMBER: 60/08855
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APPLICATION NUMBER: 60/090349
FILING DATE: 1998-06-23
APPLICATION NUMBER: 60/090355
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APPLICATION NUMBER: 60/089907
FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089908
FILING DATE: 1998-06-18
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FILING DATE: 1998-06-16
APPLICATION NUMBER: 60/089514
FILING DATE: 1998-06-16
APPLICATION NUMBER: 60/089532
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PLICATION NUMBER: 60/089538
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FILING DATE: 1998-06-19
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FILING DATE: 1998-06-19
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APPLICATION NUMBER: 60/090252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/088810
FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088824
APPLICATION NUMBER: 60/088824
FILING DATE: 1998-06-10
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FILING DATE: 1998-06-11
APPLICATION UNMBER: 60/08876
FILING DATE: 1998-06-11
APPLICATION NUMBER: 60/089105
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FILING DATE: 1998-06-17
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FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/08858
FILING DATE: 1998-06-11
APPLICATION NUMBER: 60/068033
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088326
FILING DATE: 1998-06-04
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FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088202
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1 MKLAALIGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLL 60 Gaps ; Length 104; LSSLGIPVNHLIEGSQKCVAELGPQAVGAVKALKALLGALTVFG 104 Indels 100.0%; Score 502; DB 9; 100.0%; Pred. No. 7.5e-47; Mismatches THE FILING DATE: 1998-06-24

S. APPLICATION NUMBER: 60/090557

S. APPLICATION NUMBER: 60/090557

S. PILING DATE: 1998-06-25

S. FILING DATE: 1998-06-25

S. FILING DATE: 1998-06-25

S. FILING DATE: 1998-06-25

S. APPLICATION NUMBER: 60/090690

S. APPLICATION NUMBER: 60/090690

S. APPLICATION NUMBER: 60/090690

S. APPLICATION NUMBER: 60/090695

S. FILING DATE: 1998-06-25

S. APPLICATION NUMBER: 60/090695 R FILING DATE: 1998-06-24
R APPLICATION NUMBER: 60/090535
R FILING DATE: 1998-06-24
A PPLICATION NUMBER: 60/090540
R FILING DATE: 1998-06-24
R APPLICATION NUMBER: 60/090542 APPLICATION NUMBER: 60/090435
RILING DATE: 1998-06-24
FILING DATE: 1998-06-24
FILING DATE: 1998-06-24
FILING DATE: 1998-06-24 FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091626 FILING DATE: 1998-07-02 FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091978 FILING DATE: 1998-07-07 APPLICATION NUMBER: 60/091982 FILING DATE: 1998-07-07 APPLICATION NUMBER: 60/092182 FILING DATE: 1998-07-09 APPLICATION NUMBER: 60/090445 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090472 FILING DATE: 1998-06-25 APPLICATION UNMERE: 60/090862 FILING DATE: 1998-06-26 APPLICATION NUMBER: 60/090863 FILING DATE: 1998-06-26 APPLICATION NUMBER: 60/091360 FILING DATE: 1998-07-01 APPLICATION NUMBER: 60/091478 APPLICATION NUMBER: 60/091519 APPLICATION NUMBER: 60/090429 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090431 FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091544 ; 0 FILING DATE: 1998-07-01 Conservative Query Match Best Local Similarity Matches 104; Conserv 61 PRIOR
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RESULT 14 US-09-989-293A-408 Sequence 408, Application US/09989293A ; Patent No. US20020177164A1

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E FILING DATE: 1998-06-10
E APPLICATION NUMBER: 60/088826
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E APPLICATION NUMBER: 60/088858
E FILING DATE: 1998-06-11
E FILING DATE: 1998-06-11
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R FILING DATE: 1998-06-05
R PILING DATE: 1998-06-09
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APPLICATION NUMBER: 60/089907
FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089908
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FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/089948
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FILING DATE: 1998-06-22
APPLICATION NUMBER: 60/090252
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APPLICATION NUMBER: 60/090349
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FILING DATE: 1998-06-23
APPLICATION NUMBER: 60/090429
FILING DATE: 1998-06-24
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FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088824
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APPLICATION NUMBER: 60/089105
FILING DATE: 1998-06-12
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FILING DATE: 1998-06-16
APPLICATION NUMBER: 60/089512
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FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089538
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FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089599
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APPLICATION NUMBER: 60/089600
FILING DATE: 1998-06-17
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FILING DATE: 1998-06-19
                APPLICATION NUMBER: 60/088167
FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088202
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APPLICATION NUMBER: 60/088742
FILING DATE: 1998-06-10
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FILING DATE: 1998-06-16
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APPLICATION NUMBER: 60/090254
                                                                                     FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088212
FILING DATE: 1998-06-05
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APPLICATION NUMBER: 60/089801
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THILE CF INVENTION: ACIDS ELECTRICAL CATTOR TO CURRENT APPLICATION NUMBER: US/09/989,293A CURRENT APPLICATION NUMBER: 60/049787 PRIOR APPLICATION NUMBER: 60/06250 PRIOR FILING DATE: 1997-06-16 PRIOR FILING DATE: 1997-10-17 PRIOR FILING DATE: 1997-10-17 PRIOR PILING DATE: 1997-11-13 PRIOR APPLICATION NUMBER: 60/065311 PRIOR FILING DATE: 1997-11-13 PRIOR PILING DATE: 1997-11-13 PRIOR APPLICATION NUMBER: 60/065311 PRIOR APPLICATION NUMBER: 60/065311 PRIOR PILING DATE: 1997-11-12 PRIOR PILING DATE: 1998-03-25 PRIOR PILING DATE: 1998-03-26 PRIOR PILING DATE: 1998-03-27 PRIOR PILING DATE: 1998-05-03 PRIOR PILING DATE: 1998-05-03 PRIOR PILING DATE: 1998-05-03 PRIOR PILING DATE: 1998-06-02 PRIOR PILING DATE: 1998-06-03 PRIOR PILING DATE: 1998-06-04 PRIOR PILING DATE: 1998-06-07 PRIOR PILING DATE: 1998-06-04 PRIOR
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APPLICATION UNDBER: 60/088033
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088326
                                                                                                                                                                                                                                                       Godowski, Paul J.
Grimaldi, J.Christopher
Gurney, Austin L.
Kljavin, Ivar J.
                                                                                                                                                                                                                                                                                                                                                                                                               Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
                                                                                                               Eaton, Dan L.
Ferrara, Napoleone
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Paoni, Nicholas F.
                                                                                                                                                                                                          Gerritsen, Mary E.
Goddard, Audrey
                                                                                                                                                                                    Gerber, Hanspeter
                       APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
                                                                                                                                                                                                                                                                                                                                               Napier, Mary A.
                                                                                            Desnoyers, Luc
                                                                                                                                                               Fong, Sherman
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    GENERAL INFORMATION:
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APPLICANT:
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and Transmembrane Polypeptides and Nucleic
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CURRENT APPLICATION NUMBER: US/09/989,735
PRIOR APPLICATION NUMBER: 60/049787
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R FILING DATE: 1998-06-04

R APPLICATION NUMBER: 60/088025

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R APPLICATION NUMBER: 60/088026

R FILING DATE: 1998-06-04
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REPLING DATE: 1997-10-17
REPLING DATE: 1997-10-17
REPLING DATE: 1997-11-12
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R APPLICATION NUMBER: 60/083322
R FILING DATE: 1998-04-28
R FILING DATE: 1998-04-28
R FILING DATE: 1998-06-07
R FILING DATE: 1998-06-07
R FILING DATE: 1998-07-07
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FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088029
FILING DATE: 1998-06-04
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APPLICATION NUMBER: 60/087609
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APPLICATION NUMBER: 60/087759
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APPLICATION NUMBER: 60/087827
FILING DATE: 1998-06-03
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APPLICATION NUMBER: 60/087607
                                                                                                                                                                                                                                                                                                     Grimaldi,J.Christopher
Gurney,Austin L.
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
Tumas, Daniel
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                                                                                          Ferrara, Napoleone
Fong, Sherman
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Paoni, Nicholas F.
                                                                                                                                                                                                   Gerritsen, Mary E.
                                                                                                                                                                       Gerber, Hanspeter
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100.0%; Score 502; DB 9;
Best Local Similarity 100.0%; Pred. No. 7.5e-47;
Matches 104; Conservative 0; Mismatches 0;
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PRIOR PLING DATE: 1998-06-25
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PRIOR APPLICATION NUMBER: 60/09166
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PRIOR APPLICATION NUMBER: 60/09163
PRIOR PLING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/09163
PRIOR PLING DATE: 1998-07-02
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PRIOR PRIOR DATE: 1998-07-03
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Sephication No. US20020193299A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-989-735-408
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FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088167 FILING DATE: 1998-06-05

APPLICATION NUMBER: 60/088326

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PRIOR APPLICATION NUMBER: 60/08212
PRIOR FILING DATE: 1998-06-05
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Length 104; 100.0%; Score 502; DB 9; 100.0%; Pred. No. 7.5e-47; R FILING DATE: 1998-06-24

R APPLICATION NUMBER: 60/090445

RR RILING DATE: 1998-06-24

RR APPLICATION NUMBER: 60/090472

RR RILING DATE: 1998-06-24

RR APPLICATION NUMBER: 60/090535

RR APLICATION NUMBER: 60/090540

RR APPLICATION NUMBER: 60/090540

RR FILING DATE: 1998-06-24

RR APPLICATION NUMBER: 60/090540 FILING DATE: 1998-07-07 APPLICATION NUMBER: 60/091982 FILING DATE: 1998-07-07 APPLICATION NUMBER: 60/090676
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APPLICATION NUMBER: 60/090678
FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090690 FILING DATE: 1998-07-01 APPLICATION NUMBER: 60/091478 FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/092182 FILING DATE: 1998-07-09 FILING DATE: 1998-06-25
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APPLICATION NUMBER: 60/090695
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APPLICATION NUMBER: 60/090557
FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/091626 APPLICATION NUMBER: 60/091633 APPLICATION NUMBER: 60/090696 FILING DATE: 1998-07-02 Query Match PRIOR PRIOR

1 MKLAALLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLL 1 MKLAALLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKUL Gaps ö Indels 0 0; Mismatches Best Local Similarity 100. Matches 104; Conservative

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Search completed: June 2, 2004, 20:25:21 Job time : 20.5413 secs

Run

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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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US-08-964-725-14
                                   Sequence 25696, A Sequence 21756, A Sequence 21756, A Sequence 2, Appli Sequence 34, Appli Sequence 3, Appli
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Sequence 3, Appli
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26821, A
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Sequence 12, Appl
Sequence 28114, A
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                                                                                                                                      June 2, 2004, 20:16:40 ; Search time 7.24797 Seconds (without alignments) 740.773 Million cell updates/sec
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1 MKLAALLGLCVALSCSSAAA......QAVGAVKALKALLGALTVFG 104
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                       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-196-387-2

US-09-941-835-2

US-09-972-1158-6

US-09-972-1158-6

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US-09-543-681A-4680
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Gapop 10.0 , Gapext 0.5
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Sequence 13907, A Sequence 12597, A Sequence 2, Appli Sequence 4, Appli Sequence 4, Appli Sequence 61, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli Sequence 5, Appli Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 14, Application US/08964725

Sequence 14, Application US/08964725

Patent No. 5939265

GENERAL INFORMATION:
APPLICANT: COHEN, Maurice
APPLICANT: FRIEDMAN, Paula N.
APPLICANT: HONGES, Steven C.
APPLICANT: KLASS, Michael R.
APPLICANT: KRATOCHVIL, Jon D.
APPLICANT: ROBERIS-RAPP, Lisa
APPLICANT: ROBERIS-RAPP, Lisa
APPLICANT: ROBERIS-RAPP, Lisa
APPLICANT: STROUPE, Steven D.
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE LUNG
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                          US-09-252-911A-31479
US-08-426-125-4
US-08-456-125-4
US-09-367-512-3
US-08-951-567B-61
US-09-134-000C-4469
US-09-134-000C-4469
US-09-134-000C-4469
US-09-591-079-10
US-09-591-079-10
US-09-591-079-10
US-09-370-700-5
US-09-370-700-5
US-09-603-207-5
US-09-603-207-5
US-09-603-207-5
US-09-107-532A-5682
                  US-09-489-039A-13907
                                               -09-489-039A-12597
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COUNTRY: USA
ZIP: 6004-3500
ZIP: 6004-3500
COMPUTER READABLE FORM:
WEDIUM TYPE: Diskettle
COMPUTER: IBM Compatible
CPERATING SYSTEM: DOS
SOFTWARE: FSASERQ for Windows Version 2.0
CURBINT APPLICATION DATA:
APPLICATION NUMBER: US/08/964,725
                                                                                        JS-09-647-224A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIPECATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: BECKEY, Cheryl L.
REGISTRATION NUMBER: 35,441
FREGESCHWUICATION NUMBER: 5997.US.PI
TELECOMMUICATION:
TELEPHONE: 847/935-1729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Abbott Laboratories STREET: 100 Abbott Park Road CITY: Abbott Park
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14:

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Sequence 10, Application US/09196387
Patent No. 6277613
                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/196,387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 133521
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                    STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 673 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / MOLECULE TYPE: protein US-09-841-835-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-196-387-10
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                         US-09-841-835-8
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                                                                                                          1 MKLAALLGLCVALSCS-SAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKL 59
                                                                                                                                         ------PLDNILPFMDPLKL 51
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                                                                                                                                                                                                                                                                                   Sequence 8, Application US/09196387

Patent No. 6277613

GENERAL INFORMATION:
APPLICANT: Ge Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16.5%; Score 83; DB 3; Length 673; 30.5%; Pred. No. 0.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43; Indels
                                              Length 93;
                                                                               Indels
                                                                                                                                                                             60 LLSSLGIPVNHLIEGSQKCVAELGPQAVGAVKALKALLGAL 100
                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/196,387
                                                                               38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70 HLIEGSQ----KCVAELGPQAVGAVKALKALLGAL 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 160; DB 2;
Pred. No. 1.3e-11;
                                                                                                                                           1 MKLVTIFLLVTISLCSYSATAFLINKVPLPVDKLAPL
                                                                             9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26,742
PR: 600-1-230 CIP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/095,225
FILING DATE: June 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Jackson Esg., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 600 TELECOMMUNICATION INFORMATION: TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Floppy disk
IBM PC compatible
No. 5939265e
                                              ch 31.9%;
1 Similarity 43.6%;
44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29; Conservative
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TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARATERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 673 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: protein US-09-196-387-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
GY: linear
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 411 CTTY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: PatentI
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                                                   Query Match
Best Local Similarity
   MOLECULE TYPE:
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TELEFAX: 20
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        ; MOLECULE TY:
US-08-964-725-14
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US-09-196-387-8
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90 CSTTSTICTVAAAPVV-PAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSSSSSPSSPGS 148
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APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
Sequence 8, Application US/09841835
Patent No. 6506587
GENERAL INFORMATION:
APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDERSS:
ADDRESSEB: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/841,835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70 HLIEGSQ----KCVAELGPQAVGAVKALKALLGAL 100
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CCRRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 16.5%; Score 83; DB Best Local Similarity 30.5%; Pred, No. 0.28 Matches 29; Conservative 13; Mismatches
                                                                                                                                                                                                                                                              ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NOMBER: 26,742
HEFERENCE/DOCKET NUMBER: 600-1-230 CIP1
TELECOMMUNICATION INFORMATION:
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Sequence 2, Application US/09196387

Patent No. 6277613

GENERAL INFORMATION:
APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARENTH Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/196,387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Klauber & Jackson
STREET: 411 Hackeneack Avenue, 4th Floor
CITY: Hackeneack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/095,225
FILING DATE: June 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
PREJERRATION NUMBER: 26,742
PREPERRICE/DOCKET NUMBER: 26,742
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1327 amino acids
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TELEFAX: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 133521
INFORMATION FOR SEQ 1D NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
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                                                                                                                                                                                                                                                        , MOLECULE TYPE: protein US-09-841.-835-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: New Jersey
COUNTRY: USA
ZIP: 07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 CSSAAAFLVGSAKPVAQPVAALESAA----EAGAGTLANPLGTLNPLKLLLSSLGIPVN 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10, Application US/09841835
Patent No. 6506587
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
SMith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: All Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16.5%; Score 83; DB 3; Length 949; 30.5%; Pred. No. 0.45; tive 13; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patentin Release #1.0, Version #1.30
                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/196,387 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70 HLIEGSQ----KCVAELGPQAVGAVKALKALLGAL 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          149 SLAESPEAAGVSSTAPLGPGAAGPGTGVPAVSGAL 183
                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/095,225
APPLICATION NUMBER: 0, 1998
ATTORNEY/AGENT INFORMATION:
NAME: JGCSON ESQ., David A.
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 600-1-230 CIPI
TELEPHONE: 201-4487-5800
TELEFAX: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 07601
COMPUTER: EBADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/841,835
                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/196,387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 133521
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
ERNGTH: 949 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 30.5%
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
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New Jersey
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CLASSIFICATION:
                      USA
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                    COUNTRY:
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90 CSTTSTICTVAAAPVV-PAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSSSSSPSSPGS 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
16.5%; Score 83; DB 4; Length 949;
Best Local Similarity 30.5%; Pred. No. 0.45;
Matches 29; Conservative 13; Mismatches 43; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              149 SLAESPEAAGVSSTAPLGPGAAGPGTGVPAVSGAL 183
                 NAME: Jackson Esg., David A.
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 600-1-230 CIP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5804
TELEPHONE: 201-343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 949 amino acids
TYPE: amino acid
ATTORNEY/AGENT INFORMATION:
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149 SLAESPEAAGVSSTAPLGPGAAGPGTGVPAVSGAL 183
                                                                                         ; Sequence 8, Application US/09972115A ; Patent No. 6599728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82 LGPQAVG 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-252-991A-25696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 25696
LENGTH: 718
                                                                                                                                                                                                                                                                                                                                                                                                                                     1327
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                                                            RESULT 8
US-09-97:2-115A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                     90 CSTISTICTVAAAPVV-PAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSSSSSPSSPGS 148
                                                                                                                                      15 CSSAAAFLVGSAKPVAQPVAALESAA-----EAGAGTLANPLGTLNPLKLLLSSLGIPVN 69
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                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:

APPLICANT: de Lange, Titia
APPLICANT: Swith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4; Length 1327; 0.71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43; Indels
                                                                  DB 3; Length 1327;
                                                                                                       43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 07601

CMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/841,835
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                                                                                                                                                                                                                    70 HLIEGSQ----KCVAELGPQAVGAVKALKALLGAL 100
                                                                                                                                                                                                                                                   149 SLAESPEAAGVSSTAPLGPGAAGPGTGVPAVSGAL 183
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16.5%; Score 83; DB 4
Best Local Similarity 30.5%; Pred. No. 0.71.
Matches 29; Conservative 13; Mismatches
                                                                  Query Match
16.5%; Score 83; DB 3
Best Local Similarity 30.5%; Pred. No. 0.71;
Matches 29; Conservative 13; Mismatches
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REPERENCE/DOCKET NUMBER: 600-1-TELECOMMUNICATION INFORMATION: TELEFHONE: 201-487-5800
TELEFAN: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/196,387
FILLING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09841835 Patent No. 6506587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 133521
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 1327 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein HYPOTHETICAL: NO
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STATE: New Jersey
COUNTRY: USA
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                 ; HYPOTHETICAL:
US-09-196-387-2
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Sequence 25596, Application US/09252991A

Sequence 25596, Application US/09252991A

Patent No. 6551790

General Information:
APPLICATION

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONA

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONA

TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196,136

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 CSSAAAFLVGSAKPVAQPVAALESAA-----EAGAGTLANPLGTLNPLKLLLSSLGIPVN 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16.5%; Score 83; DB 4; Length 1327; 30.5%; Pred. No. 0.71; tive 13; Mismatches 43; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31, Indels
APPLICANT: Geron Corporation
APPLICANT: Gerog, Morin B.
APPLICANT: Gregg, Morin B.
APPLICANT: Walter, Funk D.
APPLICANT: Walter, Funk D.
APPLICANT: Walter, Funk D.
TITLE OF INVENTION: A Second Mammalian Telomerase
FILE REFRENCE: 080/003C
CURRENT APPLICATION NUMBER: US/09/972,115A
CURRENT PILING DATE: 2001-10-05
PRIOR PILING DATE: 2000-04-10
PRIOR FILING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 64
SOCTIMARE: Patentin version 3.1
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ilarity 37.3%; Pred. No. 0.35;
Conservative 8; Mismatches
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35 ALESAAEAGAGTLANPLGTLNPLK-----LLLSS-----LGIPVNHLIEGSQKCV 79
Score 73.5; DB 3; Length 443;
Pred. No. 2.1;
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APPLICANT: LAL, PREETI
APPLICANT: CORLEY, NEIL C.
APPLICANT: PATTERSON CHANDRA
APPLICANT: PATTERSON CHANDRA
APPLICANT: BAUGHN, MARIAH R.
TITLE OF INVENTION: HUMAN ISOMERASE-LIKE PROTEINS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyce Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IDEN COMPATIBLE
COMPUTER: IDEN COMPATIBLE
SOFRATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible OPERATING SYSTEM: Windows SOFTWARE: FASTSEQ for Windows VereCURIENT APPLICATION DATA: US/09/088,425 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09639378A; Patent No. 6224838; GENERAL INFORMATION:
                                                                                                                                         Sequence 2, Application US/09088425; Patent No. 6171843; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C
REGISTRATION UNDRER: 39,132
REFERENCE/DOCKET NUMBER: PF-O
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-6555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 34.1%;
Matches 29; Conservative
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SEQTENCE CHARACTERISTICS:
LENGTH: 443 amino acids
TYPE: amino acid
STRANDEDNESS: single
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILLING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIBRARY: TMLR3DT01
CLONE: 289973
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US-09-639-378A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: CA
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                                                                           US-09-252-991A-21756

US-09-252-991A-21756

Sequence 21756, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICATION: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR PLILING DATE: 1998-02-18

PRIOR PLILING DATE: 1998-02-18

PRIOR PLILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 21756

LENGTH: 255

LENGTH: 255
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APPLICANT: MAC. J. Rubenfield et al.

APPLICANT: MAC. J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER: OF SEQ ID NOS: 33142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65 -LLEGLRVRPRHARPEHQVHGSDGETVGLLVEGDLGAGLDTFGGQAGLAEHHRQGHAEAA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 CLAAECCAAHPAAFDCGRPGPVRRAGEAFRSAVEAGVQADLRVEHLGYRATGLGLVGD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
15.3%; Score 77; DB 4; Length 540;
Best Local Similarity 30.0%; Pred. No. 1.1;
Matches 33; Conservative 13; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 CVALSCSSA--AAFLVGSAKPVAQPVAALESAAEAGA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.6%; Score 78.5; DB 4;
llarity 24.1%; Pred. No. 0.25;
Conservative 10; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---- FIEG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 29143, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 LLLSSLGIPVNH-----
                    198 AGPGALG 204
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US-09-252-991A-29143
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LENGTH: 540
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Matches 39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: GenBank Accession No. 6458561 95672676
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil. C.
APPLICANT: Corley, Neil. C.
APPLICANT: Baughn, Mariah R.
TILEO FOR INVENTION: HUMAN PEPTIDYL-PROLYL ISOMERSASES
FITE REFERENCE: PF-05.29-1 DIV
CURRENT APPLICATION NUMBER: US/09/639,378A
CURRENT FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: US 09/088,425
PRIOR PILING DATE: 1998-06-01
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PERL Program
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6524838 289973CD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
14.6%; Score 73.5; Di
Best Local Similarity 33.7%; Pred. No. 4.5;
Matches 28; Conservative 11; Mismatches
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APPLICANT: Scacheri, Emanuela
APPLICANT: Scacheri, Emanuela
APPLICANT: Bascchi, Antonella
APPLICANT: Hodgson, Dave
TITLE OF INVENTION: HUMAN NIMI KINASE
FILE REFERENCE: PC-0009 US
CURRENT APPLICATION NUMBER: US/09/523,849
CURRENT FILING DATE: 2000-03-13
NUMBER OF SEQ ID NOS: 39
SEQ ID NO 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35 ALESAAEAGAGTLANPLGTLNPLK-----
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Patent No. 6458561
GENERAL INFORMATION:
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Best Local Similarity 34.1%;
Matches 29; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Molteni, Angela
APPLICANT: Magnaghi, Paola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Bandman, Olga
                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
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1 MKLAALLGLCVALSCSSAAAFLVGSAKP--VAQPVAALESAAEAGAGTLANPLGTLNPLK 58
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Fatent No. 5733778

Patent No. 5733778

Patent No. 5733778

PAPLICANT: MATLASHEWSKI, Gregory

APPLICANT: MATLASHEWSKI, Gregory

APPLICANT: GENES OF LEISHMANIA WHICH ARE DIFFERENTIALLY-
ITILE OF INVENTION: EXPRESSED IN AMASTIGOTE FORM

NUMBER OF SEQUENCES:

ADDRESSER: Sim & McBurney

CITY: Toronto

STARE: Ontario

CONTRY: Canada

CONTRY: Canada

CONTRY: Canada

ZIP: M5G 1R7

COMPUTER: Floppy disk

COMPUTER: IBM PC Compatible

COMPUTER: IBM PC Compatible

COMPUTER: DEFERRATE PORM:

MEDIUM TYBE: Floppy disk

COMPUTER: IBM PC Compatible

COMPUTER: DEFERRATE PORM:

MEDIUM TYBE: Floppy disk

COMPUTER: DEFERRATE PORM:

MEDIUM TYBE: PLOPPY MISK

MEDIUM TYBE: PLO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: STEWART, Michael I.
REGISTRATION NOMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-448 MIS:bh
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15; Mismatches
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/115,987
FILING DATE: 03-SEP-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INPORMATION: (416) 595-1155
TELEFAX: (416) 595-1163
INPORMATION FOR SEQ ID NO: 3:
SEQUIENCE CHARACTERISTICS:
TYPE
TYPE
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1 Similarity 29.8%;
31; Conservative 15
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TYPE: amino acid
STRANDEDNESS: single
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Matchés 31; Conservat
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US-08-452-531-3
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AAY6675.
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Aay84288 Human sig
Aab65280 Human pRO
Abu58095 Human PRO
Abu58095 Human PRO
Abu58095 Human Rec
Abu59173 Novel hum
Abu5927 Human Rec
Abu59320 Human PRO
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Abu59320 Human PRO
Abu5926017 Human PRO
Abu59469 Novel hum
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Abu19441 Human PRO
Abu81693 Novel hum
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                                                                              502
1 MKLAALLGLCVALSCSSAAA......QAVGAVKALKALLGALTVFG 104
                                                                                                                                                                                                                                                                                                                         Description
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                      1586107 seqs, 282547505 residues
                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                             model
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ADA37919
ADA21605
ADA10392
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AAB65280
AAU86141
ABU58095
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ABU59320
ABO26017
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ABU92235
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ABU88632
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ABU13986
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Gapop 10.0 , Gapext 0.5
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genescap2000s:*
genescap2001s:*
genescap2001s:*
genescap2002s:*
genescap2003bs:*
genescap2003bs:*
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Maximum DB seq length: 200000000
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Match Length
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                                           June
                             protein
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Perfect score:
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Human	Human	Human	Human	Human	Нишап	Human	Нишап	Human	Human	Novel	Novel	Human								
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104	104	104	104	104	104	104	104	104	104	104	104	104	104	104	104	104	104	104	104	
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	
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ALIGNMENTS

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Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand; pharmaceutical; receptor immunoadhesin; gene mapping.
AAY66757 standard; protein; 104 AA.
                                                                             Membrane-bound protein PRO1245.
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98US-0087659P.
98US-0087629P.
98US-0088023P.
98US-0088023P.
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98US-0088127P.
98US-0088117P.
98US-0088134P.
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                                                        (first entry)
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10-JUN-1998;
10-JUN-1998;
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05-JUN-1998;
09-JUN-1998;
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02.JUN-1998;
02.JUN-1998;
03.JUN-1998;
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9805-0091486P.
9805-0091519P.
9805-0091628P.
9805-0091628P.
9805-0091633P.
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9805-0095318P.
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98US-0090445P.
98US-0090445P.
98US-009045P.
98US-009064P.
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04-AUG-1998;
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98US-0095929P.
98US-0096112P.
98US-00961146P.
98US-0096129P.
98US-0096728P.
98US-0096778P.
98US-0096731P.
98US-0096731P.
98US-0096731P.
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98US-0096831P.
98US-0096831P.
98US-0096831P.
98US-009693P.
98US-009693P.
98US-009695P.
98US-009695P.
98US-0097951P.
98US-0097951P.
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98US-0098525P
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99US-0115565P
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                                                                             18-AUG-1998;
18-AUG-1998;
18-AUG-1998;
18-AUG-1998;
19-AUG-1998;
20-AUG-1998;
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                                                                                                                                             26-AUG-1998
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Chen J, Yuan J; Wood WI, Baker K,

Smith V, Watanabe CK;

Goddard A, Gurney AL,

WPI; 2000-072883/06. N-PSDB; AAZ65103.

Membrane-bound proteins and related nucleotide sequences.

Claim 12; Fig 290; 822pp; English.

The invention provides membrane-bound PRO polypeptides and polynucleotides encoding them. The PRO sequences of the invention were polynucleotides encoding them. The PRO sequences of the invention were identified based on extracellular domain homology screening. The PRO sequences have homology with proteins including LDL receptors, TIE cligands and various enzymes. The membrane-bound proteins and receptor ingands and various enzymes. The membrane-bound proteins and receptor continuncadhesins, for instance, can be used as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. The PRO encoding sequences are useful as hybridization probes, in chromosome and gene mapping and in the generation of antisense RNA and DNA. PRO nucleic acid sequences will also be useful for the preparation of PRO polypeptides, especially by recombinant techniques

Sequence 104 AA;

0; Gaps 100.0%; Score 502; DB 3; Length 104; 100.0%; Pred. No. 1.4e-48; ive 0; Mismatches 0; Indels (Query Match Best Local Similarity 100. Matches 104; Conservative

9 MKLAALLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLL

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inflammation; cardiovascular disease; anticancer; anti-inflammatory;
                                                                                                                                                                                                               Tang YT,
                                                                                                                                                                                                                                                         N-PSJB; AAZ98173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 104 AA;
                                                                                               WO200000610-A2
                                                                              Homo sapiens.
                                                                                                                                                                                                                        Akerblom IE,
                                                                                                                                  25-JJN-1999;
                                                                                                                                                                   01-0CT-1998;
11-DEC-1998;
                                                                                                                                                   26-JUN-1998;
                                                                                                                                                             31-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 104;
                                                                                                                06-JAN-2000
                                                                                                                                                                                                                                Bandman 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                              disease
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                                                                                                                                            Specific Gene; LSG; Lng107; human; diagnostic marker; prognosticate;
                                                                                                                                                                                                                                                                                                                                                       The present sequence is a lung specific gene (LSG) protein Lng107 from human clone ID 586271. The LSG has high level of tissue specificity for lungs and is overexpressed in cancerous tissues. The sequence serves as a diagnostic marker for detecting, monitoring, staging and prognosticating lung cancer. The diagnosis involves comparing levels of LSG in samples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MKLAALLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; signal peptide-containing protein; HSPP; diagnosis; cancer;
                                                                                                                                                                                                                                                                                                                        A new method for diagnosing, monitoring and staging lung cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human signal peptide containing protein HSPP-65 SEQ ID NO:65
                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 502; DB 3; Length 104; 100.0%; Pred. No. 1.4e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSSLGIPVNHLIEGSQKCVAELGPQAVGAVKALKALLGALTVFG 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSSLGIPVNHLIEGSQKCVAELGPQAVGAVKALKALLGALTVFG 104
                      LSSLGIPVNHLIEGSQKCVAELGPQAVGAVKALKALLGALTVFG 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                      obtained from patient and normal control
                                                                                                                            Human lung specific gene protein Lng107
                                                                                                                                                                                                                                                                                                                                         Example 2; Page 38-39; 40pp; English.
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                                                                        AAY44458 standard; protein; 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.08;
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                                                                                                                                                                                                                                                                              Sun Y;
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                                                                                                           (first entry)
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Best Local Similarity 100.
Watches 104; Conservative
                                                                                                                                                       cancer; diagnosis.
                                                                                                                                                                                                                                                             (DIAD-) DIADEXUS LLC
                                                                                                                                                                                                                                                                              Yang F, Macina RA,
                                                                                                                                                                                                                                                                                                WPI; 2000-116320/10
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 104 AA;
                                                                                                                                                                                                                                                                                                         N-PSDB; AAZ29723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-MAY-2000
                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                        WO9960160-A1
                                                                                                                                                                                                                           12-MAY-1999;
                                                                                                                                                                                                                                            21-MAY-1998;
                                                                                                            27-MAR-2000
                                                                                                                                                                                                          25-NOV-1999
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                                                                                        AAY44458;
                                                                                                                                               Lung
                                                                                                                                                       lung
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                                                               RESULT
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AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the thuman signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have anticancer, anti-inflammatory, antimicrobial, nootropic, hepatotropic, nepatotropic, associated with decreased activity or function of HSPP. Such diseases include cell proliferation activity or function of HSPP. Such diseases include cell proliferation (including cancer), inflammation, cardiovascular, neurological, cirproductive or developmental disorders, (e.g. arteriosclerosis, corpreductive or developmental disorders, (e.g. arteriosclerosis, craftma, Crohn's disease, microbial or other infections, congestive or ischaemic heart disease, Alzheimer's, Parkinson's or Munington's diseases, Schizophrenia, ovulatory defects, muscular dystrophy). HSPP concleic acids can be used for the recombinant production of HSPP, for detecting HSPP in standard hybridisation and amplification assays (for detecting HSPP in standard hybridisation and amplification assays (for detecting HSPP in standard hybridisation and samplification assays (for detecting HSPP in therapeutics, for detecting related sequences or genetic variations, and for chromosomal mapping, HSPP are also used to raise competitive drug screens, and for purification of HSPP from natural incompanients, and for purification of HSPP from natural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKLAALLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLL 60
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antimicrobial; nootropic; neuroprotective; cardiovascular; hepatotropic; antiasthmatic; gene therapy; cell proliferation; neurological disorder; reproductive disorder; developmental disorder; arteriosclerosis; cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia; asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia; Parkinson's disease; Huntington's diseases; ovulatory defect;
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k, Hillman JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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foung J, Yue H, Patterson C, Reddy R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 LSSLGIPVNHLIEGSQKCVAELGPQAVGAVKALKALLGALTVFG 104
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Pred. No. 1.4e-48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 206; 327pp; English
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98US-0094983P.
98US-0102686P.
98US-0112129P.
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                                                                                                                                                                                                                                                     muscular dystrophy
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chromosomal and gene mapping, and in the generation of anti-sense RNA and DNA. They may also be used to produce transgenic animals which are used to develop and screen therapeutically useful reagents. The PRO nucleotide and protein sequence can be used for tissue typing and in traating cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to AAF44470 represent PGR primers and hybridisation probes used in the isolation of human PRO sequences. AAF44087 to AAF44569 and AAB55154 to AAB55300 represent human PRO Polynucleotide and protein sequences given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, PRO; benign tumour; malignant tumour; lymphoid malignancy; leukaemia; neuronal disorder; stromal disorder; blastocoelic disorder; inflammatory disorder; immune disorder; anglogenic disorder; cytostatic;
                                                                                                                                                                                                                                                                          1 MKLAALLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLL
                                                                                                                                                                                                                                                                                               Query Match
100.0%; Score 502; DB 4; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.4e-48;
Matches 104; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                              LSSLGIPVNHLIEGSQKCVAELGPQAVGAVKALKALLGALTVFG 104
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Smith V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              d A, Godowski PJ,
Pitti RM, Roy MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAUE6141 standard; protein; 104
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99US-0123972P.
99US-0133459P.
99WO-US012252.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human PRO1245 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pan J, P. Wood WI;
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                                                                                                                                                                                Sequence 104 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neuroprotective.
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Watanabe CK,
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26-JUL-1999;
28-JUL-1999;
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01-DEC-1999;
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01-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRO polynuclectides used to produce polypeptides used to target bioactive molecules such as toxins, radiolabels or antibodies, to specific cells, to cause targeted cell death.
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Paoni NF;
Wood WI;
                                                                                                                                                                                                                                                    Human; secreted and transmembrane protein; PRO; cytostatic; cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
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                Human PRO1245 (UNQ629) protein sequence SEQ ID NO:408.
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                                                                                                                       A.
                                                                                                                       AAB65280 standard; protein; 104
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99US-0143048P.
99US-0144758P.
99US-0145698P.
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2000WO-US005004.
2000WO-US005841.
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2000WO-US004341.
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20-MAR-2000; 2000WO-US007377
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11-FEB-2000; 18-FEB-2000; 05-JAN-2000; 06-JAN-2000;

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15-SEP-1999; 15-SEP-1999; 08-OCT-1999;

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Homo sapiens

02-APR-2001

AAB65280;

22-FEB-2000;

02-MAR-2000;

Zhang Z;

Hillan KJ; Stone DM;

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9805-0088029F

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                                                                                The present invention relates to the isolation of novel human PRO polypeptides and the polynucleotide sequences encoding them. The PRO polypeptides, agnists, antagonists or anti-PRO antibodies are useful for treating benign or malignant tumours (e.g. renal, kidney, bladder, breast, etc), leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypochalamic, glandular, macrophagal, stromal and blastocoelic disorders, inflammatory, immune and angiogenic disorders. The polynucleotide sequences are also useful in gene therapy. AAU86128-AAU86162 represent the human PRO polypeptides of the invention
                                                                                                                                                                                                                                                         MKLAALLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLL 60
                                                                                                                                                                                                                                                                     Thirty five nucleic acids encoding PRO polypeptides, useful for treating benign or malignant tumors, leukemias and lymphoid malignancies, inflammatory, angiogenic and immunologic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver; horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT; antibody-dependent enzyme mediated prodrug therapy.
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                                                               Claim 61; Fig 28; 302pp; English
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Matches 104; Conservative
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100.0%; Pred. No. 1.4e-48;
ttive 0; Mismatches 0;
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02-JUN-1999
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The invention describes an isolated human PRO polypeptide. The PRO colypeptides are useful in detecting PRO polypeptides in a sample, in polypeptides are useful in detecting PRO polypeptides in a sample, in in modulating at least one biological activity of a cell expressing a PRO cin modulating at least one biological activity of a cell expressing a PRO cin modulating at least one biological activity of a cell expressing a PRO cin modulating at least not biological activity of a cell expressing a PRO cin modulating cardiac insufficiency disorders. PRO1154 and PRO1186 continual captulary endothelial growth, and PRO516, PRO943, PRO628, PRO1068 or PRO535, PRO626, PRO1166, and PRO1367 induce c-fos in endothelial growth, and are thus conditions or disorders where angiogenesis would be beneficial, e-g. wound healing and antagonist of this polypeptide are useful for treating conditions or disorders where angiogenesis would be conditions or disorders where angiogenesis would be conditional growth factor (VECEF) stimulated proliferation of conditional growth and PRO1366 and PRO1184, PRO1364 and PRO1375 stimulated proliferation of mammals which would be beneficial in inhibiting tumour growth. PRO826, PRO:068, PRO1184, PRO136, and PRO:068 or PRO:068 or PRO:068, PRO:068, PRO:068 or PRO:068 or PRO:068, PRO:068, PRO:068 or PRO:068 or PRO:068, PRO:068 or Computed o
                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346 and PRO1375, which stimulate proliferation of stimulated T-lymphocytes are therapeutically useful for enhancing immune response and in cancer treatments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKLAALLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLL
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Paoni NF;
Wood WI;
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100.0%; Pred. No. 1.4e-48;
iive 0; Mismatches 0;
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28-FEB-2001; 2001WO-US006520.
01-JJN-2001; 2001WO-US017800.
20-JJN-2001; 2001WO-US019692.
29-JJN-2001; 2001WO-US021066.
09-JJL-2001; 2001WO-US021735.
28-AJG-2001; 2001US-00941992.
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ABU82685 standard; protein; 104 AA

RESULT 8 ABU82685 ID ABU82

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  Human; PRO; secreted protein; transmembrane protein; cardiac insufficiency disorders; angiogenesis; wound healing; cancerous tumour; immune response; retinal disorder; sight loss; retinitis pigmentosum; age-related macular degeneration; AMD; kidney disorder; Berger disease; nephropathy; dermatitis; herpetiformis; Crohn's disease; sports injury; arthritis.
                                                               Human secreted/transmembrane protein PRO1245.
                                                                                                                                                                                                                                                               97105-0049767P.
97105-00652186P.
9703-00653111P.
97105-0065311P.
97105-0065311P.
97105-0065311P.
97105-0065311P.
97105-0078310P.
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98105-0081021P.
98105-0088102P.
98105-0088121P.
98105-0088121P.
98105-0088121P.
98105-0088128P.
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                                        26-JUN-2003 (first entry)
                                                                                                                                                                                            US2003032023-A1.
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17-OCT-1997;
05-NOV-1997;
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13-NOV-1997;
24-NOV-1997;
25-FEB 1998;
20-MAR-1998;
07-MAY-1998;
07-MAY-1998;
02-JUN-1998;
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                  ABU82685;
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The present invention provides the human and murine uteroglobin related protein 1 (UGRP1) promoters. The sequences can be used in the diagnosis of and prediction of predisposition to respiratory disorders such as asthma. The present sequence is a protein sequence shown in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MKLAALLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; PRO; secreted; transmembrane; signal peptide; pharmaceutical; diagnostic; therapeutic; gene therapy.
                                                                                                                                                                                                                                                                                               New human UGRP1 nucleic acid, useful for diagnosing or predicting a predisposition to develop a respiratory disorder or determining the prognosis of a subject having or suspected of having a respiratory
                                                 UGRP1; human; mouse; promoter; uteroglobin related protein 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 502; DB 6; Length 104; 100.0%; Pred. No. 1.4e-48; Indels (ive 0; Mismatches 0; Indels (
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                                                                                                                                                                                                                        (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 79-80; 83pp; English.
                         Human uteroglobin related protein 2.
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                                                                                                                                                                      18-JUN-2002; 2002WO-US019456
                                                                respiratory disorder; asthma
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11-AUG-2003 (first entry)
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                                                                                                                                                                                                                                                                           WPI; 2003-184004/18.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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Pred. No. 1.4e-48;
Mismatches 0;
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100.0%; Pre
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2000WO-US000219.
2000WO-US000376.
2000WO-US003565.
2000WO-US004341.
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980S-0097974P.
980S-0097979P.
980S-009799E.
980S-0098014P.
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99US-0145698P.
99US-0146222P.
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2000WO-US006884.
2000WO-US007377.
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17-MAY-2000; 2000WO-US013705.
22-MAY-2000; 2000WO-US014042.
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99WO-US005028.
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98WO-US019437.
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Matches 104; Conservative
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18-FEB-2000;
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20-MAR-2000;
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06-JAN-2000;
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RESULT 9 AAO19895

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06-JAN-2000;
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24-NOV-1997;
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The invention discloses isolated PRO secreted/transmembrane polypeptides comprising a sequence without signal peptide and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that encoding them. The polypeptides can be used to raise antibodies that compenies to a cell expressing a PRO protein and for modulating at least molecule to a cell expressing a PRO protein and for modulating at least one biological activity of a cell. The PRO polypeptides or for modulating at least complementary as chromosome markers, or in generating probes. The PRO identification, as chromosome markers, or in generating probes. The PRO polypeptides are useful as malecular markers for protein electrophoresis, and the isolated nucleic acids may be used for recombinantly expressing those markers. The PRO polypeptides are useful in diagnostic assays for tissue typing. Anti-PRO antibodies are useful in diagnostic assays for computal sources. The sequence provides presented in Assusoric assays for natural sources. The sequence provides presented in Assusoric data for this patent is also available in electronic format from USPTO at cell at the PRO sequence. Thus
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Godowski PJ;
Paoni NF;
Wood WI;
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Matches 104; Conservative 0; Mismatches 0; Indele
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                                            2000WO-US013705.
2000WO-US014042.
2000WO-US014941.
2000WO-US015264.
2000WO-US020710.
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2001WO-US017800.
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ABU13986 standard; protein; 104 AA.

RESULT 11 ABU13986 ID ABUI

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Human, PRO polypeptide, secreted protein; transmembrane protein; genetic disorder; antibacterial; immunosuppressive.
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97US-0062260P.
97US-0065111P.
97US-0065111P.
97US-0065111P.
97US-0065711P.
97US-0066770P.
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98WO-US025108.
99WO-US000106.
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                       (first entry)
                                        Human PRO1245 polypeptide
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2000WO-US022031.
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(GETH) GENENTECH LID.

PJ; Eaton DL;
ird A, Godowski Pi
Pan J, Paoni NF;
ims PM, Wood WI; Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Roy MA, Zhang Z;

WPI; 2003-102117/09. N-PSDB; ABX64209.

Noval secreted and transmembrane polypeptide for modulating biological activity of cell expressing the polypeptide, identifying agonists or antagonists of polypeptide, and as molecular weight markers.

Claim 12; Fig 290; 649pp; English.

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Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL; Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godd Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paor Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Woc
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02-JUN 1999; 99M0-US01252.
15-SEP-1999; 99M0-US01252.
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01-DEC-1999; 99M0-US028313.
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05-JAN-2000; 2000M0-US030951.
05-JAN-2000; 2000M0-US030951.
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03-MAR-2000; 2000M0-US03137.
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20-JUN-2001; 2001WO-US021066.
09-JUL-2001; 2001WO-US021735.
28-AUG-2001; 2001US-00941992.
98US-0088810P.
98US-0088824P.
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98US-0088861P.
98US-0089105P.
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                                                                                                                                                                                                                                                                                                                   Human; secreted and transmembrane protein; cytostatic; anti-HIV; virucide; hepatotropic; antiinflammatory; neuroprotective; gene therapy; PRO; pharmaceutical; diagnostic; biosensor; bioreactor; malignancy; cancer; ovarian cancer; colorectal cancer; Kaposi's sarcoma; leukaemia; lymphoma; hepatitis B; multiple sclerosis; Crohn's disease; drug screening.
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                                                  100.0%; Score 502; DB 6; Length 104; 100.0%; Pred. No. 1.4e-48; ive 0; Mismatches 0; Indels (
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                                                                                                                                                                                                                                                                                                 Novel human secreted and transmembrane protein PRO1245.
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97US-0065218P.
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                               Sequence 104 AA;
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Godowski PJ; Paoni NF; Wood WI;

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The invention describes a new isolated nucleic acid molecule comprising the full length coding sequence of the DNA deposited with the American type Culture Collection (e.g. ATCC Deposit No. 209621, 552-PTA, 819-PTA, 209439, 201315, etc); or a sequence with at least 80% identity to a DNA encoding a PRO polypeptide. The PRO polypeptides or polynucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These cancers (e.g. ovarian cancer, colorectal cancer, Kaposi's sarcoma, lew particularly useful for detecting or treating e.g. malignancies or cancers (e.g. ovarian cancer, colorectal cancer, Kaposi's sarcoma, leukaemia or lymphoma), hepatitis B, multiple sclerossis, or Crohn's particularly as targets for therapeutic intervention in these diseases, and in the diagnostic determination of the presence of these diseases. The PRO polypeptides are also useful as molecular weight markers, or for chromosome identification. The PRO genes are useful as hybridisation probes, or for screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene therapy, particularly for the PRO particularly for the PRO particular weight markers are more contacted and transmembrane PRO polypeptide
         New genes and secreted and transmembrane polypeptides (e.g. PRO183 or PRO184), useful for treating or diagnosing e.g. ovarian cancer, Kaposi's sarcoma, leukemia, lymphoma, hepatitis B, multiple sclerosis or Crohn's
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                                                                            Claim 12; Fig 290; 663pp; English.
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17-OCT-1997;
05-NOV-1997;
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24-NOV-1997;
25-FEB-1998;
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ABU59320
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PR 02-UII-1998; 9BUS-0091628P.

PR 02-UII-1998; 9BUS-0091633P.

PR 02-UII-1998; 9BUS-0091633P.

PR 03-UII-1998; 9BUS-0091632P.

PR 03-UII-1998; 9BUS-0091632P.

PR 04-AIU-1998; 9BUS-0091632P.

PR 04-AIU-1998; 9BUS-0091632P.

PR 04-AIU-1998; 9BUS-009531B.

PR 10-AIU-1998; 9BUS-009531B.

PR 11-AIU-1998; 9BUS-009531B.

PR 11-AIU-1998; 9BUS-009531B.

PR 11-AIU-1998; 9BUS-009532P.

PR 12-AIU-1998; 9BUS-009532P.

PR 26-AIU-1998; 9BUS-009
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geretic disorder; antibacterial; immunosuppressive.
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97US-0062250P.
97US-0062186P.
97US-0065311P.
97US-006770P.
98US-0075945P.
98US-0083322P.
98US-0084600P.
98US-008160P.
99WO-US028634.
99WO-US030095.
99WO-US03011.
2000WO-US000219.
2000WO-US00376.
2000WO-US003465.
2000WO-US004341.
                                                                  2000WO-US004914.
2000WO-US005004.
2000WO-US006319.
2000WO-US006884.
2000WO-US0088439.
2000WO-US008439.
2000WO-US01376.
2000WO-US01376.
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Best Local Similarity 100.
Matches 104; Conservative
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17-OCT-1997;
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26-REB-1998;
26-FEB-1998;
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07-MAX-1998;
07-WAX-1998;
07-UN-1998;
02-UN-1998;
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20-DBC-2099;
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22-FBB-2000;
24-FBB-2000;
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20-MAR-2000;
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20-DEC-1999;
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06-JAN-2000;
11-FEB-2000;
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08-NOV-2000;
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22-FEB-2000;
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15-SEP-1999;
30-NOV-1999;
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07-OCT-1998;
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The present invention relates to the isolation of novel human PRO polypeptides, and the polynuclectide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides, for linking biological activities of cells expressing PRO polypeptides, for modulating cartivities of cells expressing PRO polypeptides, and for for indentifying agonists or antagonists. The polynuclectide sequences encoding PRO polypeptides are useful as hybridisation probes, in the preparation of PRO polypeptides, for generating transgenic animals construct hybridisation probes for mapping the construct hybridisation probes for mapping the construct hybridisation probes for mapping the construct animals, to construct hybridisation probes for mapping the construct animals, to construct hybridisation probes for mapping the construct animals, and for the genetic analysis of individuals with genetic disorders, in gene therapy, for chromosome identification, as chromosome markers, and for generating probes for PCR, Northern analysis, Southern analysis and Western analysis, BOSCSS1 represent the human PRO polypeptides of the invention. Noce: The sequence data for this patent was obtained in electronic format directly con the USPTO web site at seqdata.uspto.gov/psipsDIDENTY.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKLAALLGECVALSCSSAAAFLVGSAKPVAQPVAALESAABAGAGTLANPLGTINPLKLL 60
                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346 and PRO1375, which stimulate proliferation of stimulated T-lymphocytes and are therapeutically useful for enhancing immune responses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKLAALLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLL
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Godowski P
Paoni NF;
Wood WI;
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Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A,
Grimaldi JC, Gurney AL, Kljavin IJ, Napler MA, Pan J,
Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM,
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100.0%; Score 502; DB 6;
Best Local Similarity 100.0%; Pred. No. 1.4e-48;
Matchen 104; Conservative 0; Mismatches 0;
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                 28-FEB-2001; 2001WO-US006520.
01-UUN-2001; 2001WO-US017800.
20-UUN-2001; 2001WO-US01962.
99-UUN-2001; 2001WO-US021066.
09-UUL-2001; 2001WO-US021065.
28-AUG-2001; 2001US-00941992.
2000WO-US032678
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N-P5DB; ACD44399.
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Human, PRO; secreted; transmembrane; signal peptide; pharmaceutical; diagnostic; biosensor; bioreactor; tumour; therapeutic; colon cancer; lung cancer; breast cancer; cancer; gene therapy.

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98US-0084500P.
98US-0084600P.
98US-008760PP.
98US-008762PP.
98US-008762PP.
98US-008802BP.
98US-008802BP.
98US-008802BP.
98US-008802BP.
98US-008802BP.
98US-008802BP.
98US-008802BP.
98US-008802BP.
98US-008802BP.
98US-008812PP.
98US-008913PP.
98US-008953PP.
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20-DEC-1999; 99WO-US030911.
05-JAN-2000; 2000WO-US000219.
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99WO-US021090
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97US-0062250P.
97WO-US020069.
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9705-00653119-
9705-00667709-
9805-00759459-
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                                                                                19-NOV-2001; 2001US-00989721
                           US2002142961-A1
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07-OCT-1998;
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24-NOV-1997;
25-FEB-1998;
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28-APR-1998;
07-MAY-1998;
28-MAY-1998;
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Homo sapiens
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The invention discloses isolated PRO secreted/transmembrane polypeptides comprising a sequence without signal peptide and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that encoding them. The polypeptides (for linking a bioactive specifically bind to the PRO polypeptide, for linking a bioactive molecule to a cell expressing a PRO protein and for modulating at least one biological activity of a cell. The PRO polypeptides or polymucleotides are also useful as pharmaceuticals, diagnostics, biosensors or bioreactors, for detecting or treating e.g. tumours in mammals, e.g. humans, dogs, cats, cattle, horses, sheep, pigs, goats or rabits as targets for therapeutic intervention in certain cancers (e.g. colon, lung or breast cancers) and diagnostic determination of the presence of these cancers. The PRO polypeptides are also useful as molecular weight markers or for chromosome identification. The PRO genes are useful as hybridisation probes or for screening libraries of human colls, genomic DNA or mRNA. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. The sequences to presented in ABUS8900-ABUS9046 are the PRO polypeptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Godowski PJ;
Paoni NF;
Wood WI;
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2000WO-US020710.
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2000WO-US023522.
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0; Gaps

5; Length 104; 18; 0; Indels 9

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100.0%; Score 502; DB 6; 100.0%; Pred. No. 1.4e-48; tive 0; Mismatches 0;

Query Match 100. Best Local Similarity 100. Matches 104; Conservative

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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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- I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.

- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.

R GO; GO: 0004194; F: Peppsin A activity; IEA.

R GO; GO: 0006194; F: Peppsin A activity; IEA.

R GO; GO: 0006508; P: Peptidase activity; IEA.

R InterPro; IPR001969; Aspprotease AS.

InterPro; IPR001969; Aspprotease AS.

InterPro; IPR001041; Peptidase AI.

R PRINTS; PR00725; PEPSIN.

R PROSITE; PR00725; PEPSIN.

R PROSITE; PR0141; ASP PROTEASE; 2.

R ASPARTY Drotease: Hydrolase; Hydrolase; Roctease.

SEQUENCE 420 AA; 45374 MW; 05A1B95D68D3F495 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                       420 AA
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                                    Q9N9H3
Q805F2
Q805F2
Q95VA2
Q95CG3
Q800A0
O57H77
Q7X8H77
Q7X8H77
Q78H75
Q81K5
Q91DE2
Q91X66
Q93106
Q93106
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P70068
Q93XR0
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Q94IA2
Q8C243
Q21966
Q86QI4
Q8WR56
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 PRELIMINARY;
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01-MAR-2002 (TrEMBLrel.
01-CCT-2003 (TrEMBLrel.
                    Homc sapiens (Human)
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Prorapsin A.
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Qgdcs8 mus musculu
Qgdcs8 mus musculu
Qgjmys mus musculu
Qsjh28 brachydanio
Q8awd9 brachydanio
P87370 oncorhynchu
Qy313 drosophila
Q9dd8 brachydanio
Ogd88 chionodraco
Q9w644 hynobius le
Q8ji24 silurus aso
Q7ze4 bombyx mori
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O9uhb3 homo gapien
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1 MSPPPLLQPLILLLPLINVE.....ARTRGADLGWGETAQAQFPG
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           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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sp_unclassified:*
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P SEQUENCE FROM N.A.

**REDLINE=20461778; PubMed=10858550; Breu V., Giller T.;

**REDLINE=20461778; PubMed=10858550; Breu V., Giller T.;

**REDLINE=20461778; PubMed=10858550;

**Cloning, expression and functional characterization of rat napsin.";

**Locial Biophys. Acta 1492:207-210(2000).

**L. SIMILARITY: BELONGS TO PEFTIDASE FAMILY Al.

**RMBL; AJ251299; CAB65392.1; -..

**RMBL; AJ251299; CAB65392.1; -..

**RMSD; P00797; ZREN.**

**RMSD; P
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                                                                                    181 AHFDGILGLGFPILSVEGVRPPMDVLVEQGLLDKPVFSFYLNRDPEEPDGGELVLGGSDP
                                                                                                                                                                                                           361 LDVPPPAGPFWILGDVFLGTYVAVFDRGDMKSSARVGLARARTRGADLGWGBTAQAQFPG
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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PRINTS; PR0072; PEPSIN.
PROSTIR; PS00141; ASP PROTEASE; 2.
ASPATLY] protease; Hydrolase; Protease.
SEQUENCE 420 AA; 45629 MW; A6851C6A2F7DED7C CRC64;
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01-CCT-2003 (TrEMBLrel. 25,
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MEDLINE=2005170; PubMed=10591213;
An R., Bienkowski M.J., Shuck M.E., Miao H., Tory M.C., Pauley A.M.,
Brashier J.R., Stratman N.C., Mathews W.R., Buhl A.E.,
Brashier J.G., Parodi L.A., Heinrikson R.L., Gurney M.E.;
Tomasselli A.G., Parodi L.A., Heinrikson R.L., Gurney M.E.;
"Membrane-anchored aspartyl protease with Alzheimer's disease beta-secretase activity.";
"Mature 402:337(1999).
"Is IMILARITY: BELONGS TO PEPTIDASE FAMILY Al.
EMBL; AF200344; AAF17080.1; -.
BREL; AF200344; AAF17080.2; -.
BREL; AF200345; PROTEASE; 2.
BRINTS; PRO0124; ASP PROTEASE; 2.
BRENTYS; PRO0134; ASP PROTEASE; 3.
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               PGDKPI FVPLSNYRDVQYFGEIGLGTPPQNFTVAFDTGSSNLWVPSRRCHFFSVPCWLHH
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Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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84.3%; Score 1887; DB 4; Length 450;
Best Local Similarity 85.7%; Pred. No. 3.4e-143;
Matches 360; Conservative 16; Mismatches 44; Indels
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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29 55 119

45504 MW; 715EC5472280003B CRC64;

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419 AA;
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MEDLINE=2108566; PubMed=11217851;

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Alzawa M., Mishi K., Kyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Baralov S., Casavant T., Rochi P., Lewis S., Marsuo Y., Nikaido I., Pesole G., Quackenbush J., Rochi P., Lewis S., Marsuo Y., Nikaido I., Pesole G., Quackenbush J., Rochi P., Lewis S., Marsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L., Staubli F., Sizuki R., Tomita M., Magner L., Washio T., Schriml L., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaetts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Masshiaki Y., Rawai Y., Kawaji H., Kohtsuki S., Hasseshaki Y., Rawai Y., Kawaji H., Kohtsuki S., Haysehizaki Y., Lee H., Lee H., Marki M., Handelli M., Rawai Y., Kawaji H., Kohtsuki S., Haysehizaki Y., Lee H., Marki Y., Marshia Y., Kawai Y., Lee H., 
                                                                                                                                                                                                                                            ALDVPPPAGPFWILGDVFLGTYVAVFDRGDMKSSARVGLARARTRGADLGWGETAQAQF- 418
                                                                                                                                                                                                                                                                 300 HAAIGGIPLLAGEYIILCSEIPKLPAVSFLLGGVWFNLTAHDYVIQTTRNGVRLCLSGFQ 359
                     239
                                          176 LARFDGILGLGFFPTLAVGGVQPPLDALVEQRILLEKPVFSFYLNRDSEGSDGGELVLGGSD 235
                                                                                          PAHYIPPLIFVPVTVPAYWOIHMERVKVGPGLTLCAKGCAAILDTGTSLITGPTEEIRAL 299
                                                                                                                                                                                        FAHFDGILGLGFPILSVEGVRPPMDVLVEQGLLDKPVFSFYLNRDPEEPDGGELVLGGSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Functional annotation of a full-length mouse cDNA collection.";
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GO; GO:0004194; F:pepsin A activity; IEA.
GO; GO:0008133; F:peptidase activity; IEA.
GO; GO:0008508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR001969; Aspprotease_AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Kidney-derived aspartic protease-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 409:685-690(2001).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A.
EMBL; AKO02520; BAB22158.1; --
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PRINTS; PR00792; PEPSIN.
PROSITE, PS00141; ASP PROTEASE; 2.
Aspartyl protease; Hydrolase; Protease.
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IPR009007; Pept A acid.
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                                                                                                                                                                                                                          64 KPIFVPLSNYRDVQYFGELGLGTPPQNFTVAFDTGSSNLWVPSRRCHFFSVPCWLHHRFD 123
                                                                                                                                                                                                                                                                                  59 NPSFVPLSKFMNTQYFGTIGLGTPPQNFTVVFDTGSSNLWVPSTRCHFFSLACWFHHRFN 118
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Takenaka M., Imai E., Kaneko T., Ito T., Moriyama T., Yamauchi A.,
Hori M., Kawamoto S., Okubo K.;
Isclation of genes identified in mouse renal proximal tubule by
comparing different gene expression profiles.";
Kidney Int. 53:562-572(1998).
-! SIMILARITY: BELONGS TO PEPTIDASE FAMILY Al.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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        11; Length
ch 69.3%; Score 1551.5; DB 11; Lengt
11 Similarity 70.1%; Pred. No. 2.7e-116;
295; Conservative 37; Mismatches 80; Indels
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Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
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HSSE; P00797; ZREN.
MGD; MGI:109345; Kdap.
GO; GO:0004194; F:pepsin A activity; IEA.
GO; GO:0008233; F:peptidase activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Aspartic proteinase family member similar to renin.
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TISSUE=Kidney;
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Query Match
Best Lccal Similarity
Matches 205; Conserv
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TISSUE=Kidney
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                                                                                                                                                                                                                                                                                                                                                                                                                                     PKASSSFQANGTKFALQYGTGRVDGILSEDKLTIGGIKGASVIFGEALWEPSLVFAFAHF 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244 IPPLTFVPVTVPAYWQIHMERVKVGPGLTLCAKGCAAILDTGTSLITGPTEEIRALHAAI 303
                                                                                                                                                                                                                                                                                                                                                       64 KPIFVPLSNYRDVQYFGEIGLGTPPQNFTVAFDTGSSNLWVPSRRCHFFSVPCWLHHRFD 123
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria, Squamata, Scleroglossa, Scincomorpha, Lacertoldea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               De Stamio R., Borrelli L., Kille P., Parisi E., Filosa S.; "Isolation, Characterization and Molecular Cloning of Cathepsin Lizard Ovary: Changes in Enzyme Activity and mRNA Expression Throughout Ovarian (Cycle."; Mol. Reprod. Dev. 52:126-134 (1999).
                                                                                                                                                                                   69.3%; Score 1550.5; DB 11; Length 419; 70.1%; Pred. No. 3.3e-116;
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Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
                                                        Pfam; PF00026; asp; 1.
PRINTS; RR00792; PEBSIN.
PROSTITE; PS00141; ASP PROTEASE; 2.
ASPARTY] Drotease; Hydrolase; Protease.
SEQUENCE 419 AA; 45500 MM; 552D2468B71B320F CRC64;
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Last annotation update)
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                                                                                                                                                                                                      ; Pred. No. 3.3e-116; 37; Mismatches 80;
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InterPro; IPR001969; Aspprotease AS.
InterPro; IPR001461; Peptidase AI.
InterPro; IPR009007; Pept_A_acid.
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TISSUE-Ovary;
MEDLINE-99105748; PubMed-9890742;
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                                                                                                                                                                                                             Best Local Similarity ,....
Matches 295; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          233 FGGVDPQYYTGDFTWVNVTRKAYWQIHMEKVDVDNGLTVCKDGCEA1VDFGTSLITGFTD 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        295 BIRALHAAIGGIPLLAGEYIILCSEIPKLPAVSFLLGGVWFNLTAHDYVIQTTRNGVRLC 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -LGAPSPGDKPIFVPLSNYRDVQYFGEIGLGTPPQNFTVAFDTGSSNLWVPSRRCHFFSV 114
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Briggs J.P.;
"Cathepsin D is Responsible for Angiotensin Generation in Zebrafish.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AYOE0516; AAL61540.1;
O), GO:0004192; F:cathepsin D activity; IEA.
GO; GO:0016787; F:hydrolase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    115 PCWLHHRFDPKASSSFQANGTKFALQYGTGRVDGILSEDKITIGGIKGASVIFGEALWEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            235 LGGSDPAHYIPPLTFVPVTVPAYWQIHMERVKVGPGLTLCAKGCAAILDTGTSLITGPTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 LQPLILLLELENVEPSGATLIRIPLHRVQPGRRTL----NLLRGWREPAELPK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        175 SLVPAPAHFDGILGLGFPILSVEGVRPPMDVLVEQGLLDKPVFSFYLNRDPEBPDGGELV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae, Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26;
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                                                                                 MEROPS; A01.009; -.

GO; GO:0004194; F:pepsin A activity; IEA.

GO; GO:0008233; F:peptidase activity; IEA.

GO; GO:00056208; F:proteclysis and peptidolysis; IEA.

InterPro; IPR001969; Asprotease_AS.

InterPro; IPR001961; Peptidase_AI.

InterPro; IPR00305; asp; 1.

PRINTS; PR00792; PEPSIN.

PRINTS; PR00792; PEPSIN.

PROSITE; PS00141; ASP PROTEASE; 2.

ASPART, Jrotease; Hydrolase; Protease.

SEQUENCE 399 AA; 43256 MW; B625C0E8F899AFE3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Cathepsin D precursor (EC 3.4.23.5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           45.8%; Score 1025; DB 13;
ilarity 50.4%; Pred. No. 5e-74;
Conservative 63; Mismatches 113;
-i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY Al.
EMBL; AJ009838; CAA08878.1; -.
HSSP; P07339; 1LYB.
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78 YFGEIGLGTPPQNFTVAFDTGSSNLWVPSRRCHFFSVPCWLHHRFDPKASSSFQANGTKF 137
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                                                                                                                                                                                                                                                                                                                                                                                                  316 KKVPILPTISFSLGGKVYSLTGEQXILKESQGGHDICLSGFMGLDIPPPAGPLMILGDVF 375
                                                                                                   26 LIRIPLHRVQPGRRTLNLLRGWREPAELP-----KLGAPSPGDKPIFVPLSNYRDVQ
                                                                                                                                                                                                                                                                                                     GVRPPMDVLVEQGLLDKPVFSFYLNRDPEEPDGGELVLGGSDPAHYIPPLTFVPVTVPAY
                                                                                                                                                                                                                                                                                                                          196 GVPPVFDMMMSQKKVEKRVPSPYLNRNPDTQPGGBLLLGGTDPKYYTGDFNYVDISRQAY
                                                                                                                                                                                                                                                                                                                                                                             WOIHMERVKVGPGLTLCAKGCAAILDTGTSLITGPTEEIRALHAAIGGIPLLAGEYIILC
                                                                                                                                                                                                                                                                                                                                                                                                                                                       318 SEIPKLPAVSFLLGGVWFNLTAHDYVIQTTRNGVRLCLSGFQALDVPPPAGPFWILGDVF
                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Cathepsin D (EC 3.4.23.5).
Cathepsin D (EC 3.4.23.5).
Eukaryotus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryotus, Metazoa; Chordata; Cremiata; Verfebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

1850D=Pre-vitellogenic ovary;

MEDLINE-98072428; Pubmed-9409770;

Brooks S., Tyler C.R., Carnevali O., Coward K., Sumpter J.P.;

Molecular characterisation of ovarian cathepsin D in the rainbow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45.3%; Score 1014.5; DB 13; Length 398; 50.6%; Pred. No. 3.4e-73;
     DB 13; Length 398;
                                          15;
                       Pred. No. 1.6e-73;
65; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE, PS00141; ASP PROTEASE; 2.
Aspartyl protease; Hydrolase; Protease.
SEQUENCE 398 AA; 42973 MW; 23C94FB3F5EC99D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO: 0004192; F:cathepsin D activity; IEA.
GO; GO:0004194; F:pepsin A activity; IEA.
GO; GO:0004331; F:peptidase activity; IEA.
GO; GO:0006508; P:proteclysis and peptidolysis; IEA.
InterPro; IPR001969; Aspprotease_AS.
InterPro; IPR001461; Peptidase_AI.
InterPro; IPR009007; Pept_A_acid.
Pfam; PF00026; asp; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY AL. EMBL; U90321; AAC60301.1; -. HSSP; P07339; 1LYB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               398 AA
   45.5%; Score 1018.5;
50.5%; Pred. No. 1.6e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 378 LGTYVAVFDRGDMKSSARVGLARART 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  trout, Oncorhynchus mykiss.";
Gene 201:45-54(1997).
                     50.5%;
                       Best Local Similarity 50.5
Matches 195; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00792; PEPSIN.
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Best Local Similarity
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       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     138 AIQYGTGRVDGILSEDKLTIGGIKGASVIFGEALWEPSLVFAFAHFDGILGLGFPILSVE 197
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                                                                                                                                                                                                                                                                                                                                                                           YFGEIGLGTPPQNFTVAFDTGSSNLWVPSRRCHFFSVPCWLHHRFDPKASSSFQANGTKF
                                                                                                                                                                                                                                                                                                     26 LIRIPLHRVQPGRRTLNLLRGWREPAELP-----KLGAPSPGDKPIFVPLSNYRDVQ
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii; Teleostei; Ostariophysi, Cypriniformes;
                                                                                                                                                                                                                           DB 13; Length 398;
                                                                                                                                                                                                                                                                15;
                                                                                                                                                                                                                         45.5%; Score 1018.5; DB 13; Length
50.5%; Pred. No. 1.6e-73;
.ive 65; Mismatches 111; Indels
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Strausberg R.,
Sthomitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC0421316; AAH42216.1;
GO; GO:0004194; F:pepsin A activity; IEA.
GO; GO:000508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR001595; Aspprocease AS.
InterPro; IPR001461; Peptidase AI.
InterPro; IPR009007; Pept_A acid.
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2A42FE4239B897F6 CRC64;
GO; GO:0004194; F:pepsin A activity; iss.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR001969; Aspprotedase AS.
InterPro; IPR001461; Peptidase AI.
InterPro; IPR009007; Pept A_acid.
PFam: PF00026; asp; 1.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                       PEAN; PF00026; asp; 1.
PRINTS; PR00792; PEPSIN.
PROSITE; PS00141; ASP_PROTEASE; 2.
                                                                                                                                                                                      43171 MW;
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Best Local Similarity 50.59
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                                                                                                                                                                       18
                                                                                                                                                                                        398 AA;
                                                                                                                                                 Signal; Hydrolase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cyprinidae; Danio.
NCBI_TaxID=7955;
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adamstides P.G., Scherer S.E., Li P.W., Hookins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Li P.W., Hookins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
A brid G.C., Baxer E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Abril J.F., Agbayani A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Cawles P.V., Berman B.P., Bhandari D., Bolshakov S.,
Barkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
R. Cherry J.M., Cawley S., Dankle C., Davenport L.B., Davies P.,
R. Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
R. Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
R. Dodson K., Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
R. Glodek A., Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
A Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Alalali M., Kalush P., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
A Liasko P., Lei Y., Li J., Li Z., Liang Y., Lin X.,
R.A. Liasko P., Lei Y., Motherson D.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Morreli A.,
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                                                                                                                                AIQYGTGRVDGILSEDKLTIGGIKGASVIFGEALWEPSLVFAFAHFDGILGLGFPILSVE 197
                                                                                                                                              GVRPPMDVLVEQGLLDKFVFSFYLNRDPEBPDGGELVLGGSDPAHYIPPLTFVPVTVPAY 257
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                                                  19 LVRIPLRKFRSIRRTLTDSGRAABELLAG-QEHTKYNNLGFPSSSNGPTPETLKNFMDAQ 77
                                                                                                                                                                                                   LIRIPLHRVQPGRRTL------NLLRGWREPAELPKLGAPSPGDKPIFVPLSNYRDVQ
                                                                            78 YFGEIGLGTPPQNFTVAFDTGSSNLWVPSRRCHFFSVPCWLHHRFDPKASSSFQANGTKF
  Gaps
 13;
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Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
Mismatches 113;
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                                                                                                                                                                                                                                                                                                                                                LGTYVAVFDRGDMKSSARVGLARAR 402
                                                                                                                                                                                                                                                                                                                                                                         378 IGQYYTVFDR----DNNRVGFAKSK 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
  64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CG1548 protein (SD07085P).
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Berkeley;
  195;
                                                                                                                                                                                                                                                                                                                                                378
                          56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                     198
                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9V313
Q9V313;
  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 139 IQYGTGRVDGILSEDKLTIGGIKGASVIFGEALWEPSLVFAFAHFDGILGLGFPILSVEG 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       199 VRPPMDVLVEQGILDKPVFSFYLNRDPEEPDGGELVLGGSDPAHYIPPLTFVPVTVPAYW 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EIPKLPAVSFLLGGVWFNLTAHDYVIQTTRNGVRLCLSGFQALDVPPPAGPFWILGDVFL 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Recese M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
Sylerkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Xacheng X.H., Zhong F.N., Zhong W., Zhan M., Zhang G., Zhang E.,
Chibs R.A., Myers E.W., Rubin G.M., Venter J.C.;
The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [3] SEQUENCE FROM N.A.

Stableton M., Brokstein P., Hong L., Agbayani A., Carlson J., Stableton M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R., A Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., A Yu.C., Lewis S.E., Rubin G.M., Calniker S., Phouanenavong S., Wan K., Yu.C., Lewis S.E., Rubin G.M., Calniker S., Lomitard (Aug-2001) to the EMBL/GenBank/DbBJ databases.

I. SIMILARIY: BELONGS TO PEPTIDASE FAMILY AI.

REMBL; AR003839; AAF23824.1; -.

REMBL; AR003839; AAF33824.1; -.

REMBL; AR003839; LYB.

RESSP, PO7339; LYB.

RESSP, PO7339; LYB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QIHMERVKVGPGLTLCAKGCAAILDTGTSLITGPTEEIRALHAAIGGIPLLAGEYIILCS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 1005.5; DB 5; Length
; Pred. No. 1.8e-72;
56; Mismatches 112; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page-McCaw A.W., Tsang G., Rubin G.M., ", ", "sopposite a December of the Cathepsin D.", Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00792; PEPSIN.
PROSITE; PS00141; ASP PROTEASE; 2.
ASPARTAL protease; Hydrolase; Protease.
ASDURNCE 392 AA; 42472 MW; 02227F5C09BB43F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0004194; F:pepsin A activity; IEA.
GO; GO:0004231; F:peptidase activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR001969; Aspprotease AS.
InterPro; IPR001461; Peptidase AI.
InterPro; IPR00107; Pept_A_acid.
Ffam; PF00026; asp; 1.
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Matches 191; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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378 LGTYVAVFDRGDMKSSARVGLARART 403
                                                                                                                                                                                                                                          Created)
                                 377 IGQYYTVFDR----ENNRVGFAKAKS
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                                                                                                                                                                                                                                     01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 3
396 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                           093428
                                                                                                                                       RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 GEIGLGTPPQNFTVAFDTGSSNLWVPSRRCHFFSVPCWLHHRFDPKASSSFQANGTKFAI 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QYGTGRVDGILSEDKLTIGGIKGASVIFGEALWEPSLVFAFAHFDGILGLGFPILSVEGV 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            197 PPVFDMAMSQKKVEKNVFSFYLNRNPDTQPGGELLLGGTDPKYYTGDFNYVDISRQAYWQ 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            260 IHMERVKVGPGLTLCAKGCAAILDTG--TSLITGPTEEIRALHAAIGGIPLLAGEYIILC 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |||::::|||:|||:||||::||
IHMDGMSIGSGLSLCKGGCEAIVDTGTSTSLITGPAAEVKALQKAIGAIPLMQGEYMVDC 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28 RIPLHRVOPGRRTINLIRGWREPAELP-----KLGAPSPGDKPIFVPLSNYRDVQYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 RIPLKKFRTLRRTLS--DSGRSLEELVSSSNSLKYNLGFPASND-PTPETLKNYLDAQYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RPPMDVLVEQGLLDKPVFSFYLNRDPEEPDGGELVLGGSDPAHYIPPLTFVPVTVPAYWQ
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                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Noopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20570889; PubMed=11137292; Riggio M., Scudiero R., Filosa S., Parisi E.; Riggio M., Scudiero R., Filosa S., Parisi E.; Scudiero R., Filosa S., Parisi E.; Gendero R., Filosa S., Parisi E.; Gendero R., Filosa S., Parisi E.; Gendero R., Filosa S., Filosa S., Gendero R., Filosa S., Gendero R., Filosa S., Filosa S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 13; Length 399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44.9%; Score 1005.5; DB 13; Lengt
50.8%; Pred. No. 1.8e-72;
.ive 62; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PRO0792; PEPSIN.
PROSITE; PS00141; ASP PROTEASE; 2.
Aspartyl protease; Hydrolase; Protease.
SEQUENCE 399 AA; 43505 WW; 5A988CA975IBSEEC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZEIN; ZDB-GERRE-010131-8; ctsd.
GO; GO: 0004192; F: cathepsin D activity; IEA.
GO; GO: 0004192; F: cathepsin A activity; IEA.
GO; GO: 0006233; F: peptidase activity; IEA.
GO; GO: 0006508; P: proteolysis and peptidolysis; IEA.
InterPro; IPR001969; Aspprotease AS.
InterPro; IPR001461; Peptidase AI.
InterPro; IPR009007; Peptidase AI.
InterPro; IPR009007; Peptidase AI.
PFGMN; PF00026; asp; 1.
                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
01-0CT-2003 (Designe (EC 3.4.23.5).
CTSD OR CATHERSTN D.
Brachydanio rerio (Zebrafish) (Danio rerio).
                                                                                                                                                                                                                    399 AA
                                      GTYVAVFDRGDMKSSARVGLARAR 402
                                                                     373 GKYYTEFDMG----NDRVGFADAK 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                          690060
                                                                                                                                                                   RESULT 11
Q9DD89
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SO OR SO OR

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EEIRALHAAIGGIPLLAGEYIILCSEIPKLPAVSFLLGGVWFNLTAHDYVIQTTRNGVRL 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 LILL-----LPLINVEPSGATLIRIPLH------RVQPGRRTLNLLRGWREPAEL 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58 PASNAPTP----ETLKNYLDAQYYGEIGLGTPPQPFTVVFDTGSSNLWVPSIHCSLLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           114 VPCWLHHRFDPKASSSFQANGTKFALQYGTGRVDGILSEDKLTIGGIKGASVIFGEALWE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      174 PSLVFAFFAHFDGILGLGFPILSVEGVRPPMDVLVEQGLLDKPVFSFYLNRDPEEPDGGEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 MLLCVFSALALTNDAACSNSLKEIPFHQTSADRLWEESRGAPGRPSLPEVQ----LSF
                                                                                                             Cathepsin D precursor.
Chiepsin Metacasi (Antarctic teleost icefish).
Actinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei, Actinopterygii, Reprecygii, Percomorpha, Perciformes, Notothenioidei, Channichthyidae, Chionodraco.
NCBI_TaxID=36188;
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84.0%; Score 985.5; DB 13; Length 396;
Best Local Similarity 47.7%; Pred. No. 7.3e-71;
Matches 195; Conservative 62; Mismatches 121; Indels 31;
                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Liver;
MEDLINE=99227072; PubMed=10209280;
AGDASSO C., Lees W.E., Capasso A., Scudiero R., Carginale 'Kille P., Kay J., Parisi E.;
"Cathepsin D from the liver of the antarctic icefish Chiom hamatus exhibits unusual activity and stability at high
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62DAF23CCDCF805A CRC64;
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GO; GO:0004194; F:pepsin A activity; IEA.
GO; GO:0008233; F:peptidase activity; IEA.
GO; GO:0008508; P:percteolysis and peptidolysis; IEA.
InterPro; IPR001969; Aspprotease AS.
InterPro; IPR001461; Peptidase AI.
InterPro; IPR0010077; Peptidase AI.
                                                                                       Last sequence update)
Last annotation update)
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PRINTS; PRO0792; PEPSIN.
PROSITE; PSO0141; ASP PROTEASE; 2.
Agpartyl protease; Hydrolase; Protease; Signal.
18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochim, Biophys. Acta 1431:64-73(1999).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY Al.
EMBL, AJ007878; CAA07719.1; -.
HSSF; P07339; 1LYB.
396 AA.
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SDPAHYIPPLIFVPVTVPAYWQIHMERVKVGPGLTLCAKGCAAILDTGTSLITGPTEEIR 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
histone H2A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LHHRFDPKASSSFQANGTKFAIQYGTGRVDGILSEDKLTIGGIKGASVIFGBALWEPSLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAFAHFDGILGLGFFILSVEGVRPPMDVLVEQGLLDKPVFSFYLNRDPEEPDGGELVLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               298 ALHAAIGGIPLLAGEYIILCSEIPKLPAVSFLLGGVWFNLTAHDYVIQTTRNGVRLCLSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58 APSPGDKPIFVPLSNYRDVQYFGFIGLGTPPQNFTVAFDTGSSNLWVPSRRCHFFSVPCW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 LILLIPLINVEPSGATLIRIPLHRVQPGRRTIN-----LLRGWREPABLPKLG----
                                                                                                                                                 QBJIJ4;
01-CCT-2002 (TrEMBirel. 22, Created)
01-CCT-2003 (TrEMBirel. 22, Last sequence update)
01-CCT-2003 (TrEMBirel. 25, Last sequence update)
Cathepain D preproprotein.
Silurus asotus (Namazu) (Amur catfish).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
Siluridae; Silurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cho J.H., Park I.Y., Kim H.S., Lee W.T., Kim M.S., Kim S.C.;
T "Cathepsin D produces antimicrobial peptide parasin I from hist
T in the skin mucosa of fish.";
FASEB J. 16:429-431 (2002).
R MBL; AF396662; AAM62283.1;
R GO; GO:00004194; F:pepsin A activity; IEA.
R GO; GO:00006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR001469; Aspprotease AS.
InterPro; IPR001407; Peptidase AI.
InterPro; IPR001969; Aspprotease AS.
InterPro; IPR001969; Aspprotease AS.
R InterPro; IPR001969; Aspprotease AS.
R InterPro; IPR001969; Peptidase AI.
R PRINTS; PR007907; Pept A_acid.
R PRINTS; PR00792; PEPSIN.
R PRINTS; PR00792; PEPSIN.
R PRINTS; PR00792; PEPSIN.
R PRINTS; PR007941; ASP PROTEASE; 2.
R PROSITE; PS00141; ASP PROTEASE; 2.
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359 MDIPPPSG-LWTLGDVFIGPYYTVFDR----ENDRVGLAKAK 395
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Last sequence update)
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48.3%; Pred. No. 6.1e-70;
iive 66; Mismatches 119;
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MEDLINE=21863985; PubMed=11821259;
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Q721E4;
01-OCT-2003 (TEMBLrel. 25,
01-OCT-2003 (TEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 48.3
                                                                                                                                                                                                                                                                                                                                                                                              NCB1_TaxID=30991;
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                                                                                RESULT 14
Q8JI24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59 KTQQPTPEILKNYLDAQYYGEICIGTPPQCFTVVFDTGSSNLMVPSVHCSLLDIACLVHP 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 RFDPKASSSFQANGTKFALQYGTGRVDGILSEDKLTIGGIKGASVIFGEALWEPSLVFAF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70 -----LSNYRDVQYFGEIGLGTPPQNFTVAFDTGSSNLWVPSRRCHFFSVPCWLHH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28
          VEVKALQKAIGAFPLIQGEYMVNCDTVPSLPVISFTVGGQVYTLTGEQYILKVTQAGKTM 351
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Cathersin D (EC 3.4.23.5).
Hynobius lecchii (Korean salamander).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Cryptobranchoidea; Hynobiidae; Hynobius.
NCBI_TAXID=113391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AHFDGILGLGFPILSVEGVRPPMDVLVEQGLLDKPVFSFYLNRDPEEPDGGELVLGGSDP
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WEDGUENCE FROM N.A.

WEDGUENCE 20358712; PubMed=10902906;

MEDLINE=20358712; PubMed=10902906;

A Ju B.G., Kim W.S.;

R. Cloning of a cDMA encoding cathepsin D from salamander, Hynobius

R. Cloning of a cDMA encoding cathepsin D from salamander, Hynobius

R. Juna Seq. 112-28 (2000).

C -1 - SIMILARITY: BELONGS TO PEPTIDASE FAMILY Al.

DR RED, AFT15925; AAD33219.1; --

DR RESP; P07339; 1LYB.

DR RESP; P07339; 1LYB.

DR GO; C0004194; F:peptidase activity; IEA.

DR GO; C00004194; F:peptidase activity; IEA.

DR GO; C00006508; P:proteolysis and peptidolysis; IEA.

DR GO; C0006508; P:proteolysis and peptidolysis; IEA.

DR InterPro; IPR001969; Aspprotease AS.

InterPro; IPR001961; Peptidase AI.

RILEFPRO; IPR001961; Peptidase AI.

RILEFPRO; IPR0019007; Pept_Aacid.
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                                                                                           Length 397;
                                                                   CLSGFOALDVPPPAGPFWILGDVFLGTYVAVFDRGDMKSSARVGLARAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE, PS00141; ASP PROTEASE; 2.
Aspartyl protease; Hydrolase; Protease.
SEQUENCE 397 AA; 42855 MW; 75CB1EA482D3DFE9 CRC64;
                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 43.7%; Score 977; DB 13; Sest Local Similarity 48.3%; Pred. No. 3.5e-70; Matches 194; Conservative 70; Mismatches 116;
                                                                                                                                                                                                                                               397 AA
                                                                                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                  PRELIMINARY:
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PRINTS; PR00792; PEPSIN.
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01-NOV-1999
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312 EYIILCSEIPKLPAVSFLLGGVWFNLTAHDYVIQTTRNGVRLCLSGFQALDVPPPAGPFW 371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 ANGTQFAIQYGSGSLSGFLSTDDVTVGGLKVRRQTFAEAVSEPGLAFVAAKFDGILGMAF 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       298 QYAVDCSLIPHLPRVTFTIAGNDFTLEGNDYVLRVAQMGHTVCLSGFMALDVPKPMGPLW 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            132 ANGTKFALQYGTGRVDGILSEDKLTIGGIKGASVIFGEALWEPSLVFAFAHFDGILGLGF 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    192 PILSVEGVRPPMDVLVEQGLLDKPVFSFYLNRDPEEPDGGELVLGGSDPAHYIPPLTFVP 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       252 VIVPAYWQIHMERVKVGPGLTLCAKGCAAILDIGTSLITGPTBEIRALHAAIGGIPLLAG 311
                                                                                                                                                                                                                                                                                                                                                                                                                         72 NYRDVQYFGEIGLGTPPQNFTVAFDTGSSNLWVPSRRCHFFSVPCWLHHRFDPKASSSFQ 131
                                                                                                                                                                                                                                                                                                                                                                           19 VEPSGATLIRIPLHRVQPGR-----RTINLLRGWREPAELPKGGAPSPGDKPIFVPLS 71
              Cathepsin D. Bombyx moril (Silk moth).
Bombyx mori (Silk moth).
Bukaryota; Metazaa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
Bombycidae; Bombyx.
                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                     SEQUENCE FROM N.A. Gui Z., Lee K.S., Kim S.R., Jin B.R., Sohn H.D.; "CDNA sequence of a novel cathepsin D from the silkworm, Bombyx
                                                                                                                                                                                                                                                                                                                   21;
                                                                                                                                                                                                                                                                            43.2%; Score 966.5; DB 5; Length 385; 50.0%; Pred. No. 2.4e-69; Live 57; Mismatches 113; Indels 21
                                                                                                                                                                                         mori..;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY297160; AAPS0847.1; -.
SEQUENCE 385 AA; 41448 WW; 5D8FEFDA385C8937 CRC64;
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        372 ILGDVFLGTYVAVFDRGDMKSS 393
                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 50.0%
Matches 191; Conservative
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Search completed: June 2, 2004, 20:21:29 Job time: 69.3906 secs н

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                  Copyright
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 protein search, using sw model OM protein Run on:

June 2, 2004, 20:05:19; Search time 16.3371 Seconds (without alignments) 1338.637 Million cell updates/sec

8-077-00-70-SD Perfect score: Title:

1 MSPPPLLLQPLLLLLPLLINVE.....ARTRGADLGWGETAQAQFPG 420 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 141681 segs, 52070155 residues Searched:

141681

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

SwissProt 42:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	O96009 homo savien	mus mus		clupea		rattu	_	pog	Q03168 aedes aegyp		Q9mzs8 ovis aries	P70269 mus musculu	P14091 homo sapien		P43159 oryctolagus		P00796 mus musculu	cavia	oryza	P06281 mus musculu	P52115 ovis aries	P40782 cynara card	rattu		pan t		004057 cucurbita p	macaca fus	P11489 macaca mula	P00790 homo sapien	_	P55956 caenorhabdi	P03954 macaca fusc
SUMMARIES	ei ei	NAP1 HUMAN	KDAP MOUSE	CATD_CHICK	CATD_CLUHA	CATD HUMAN	CATD_RAT	CATD MOUSE	CATD_BOVIN	ASPP_AEDAE	CATD_PIG	CATD_SHEEP	CATE MOUSE			CATE RABIT	ASPR_HORVU	RENS_MOUSE	- 1	APR1_ORYSA				RENI_RAT		RENI_PANTR	ASPR_ORYSA	ASPR CUCPE	PEP4 MACFU	PEPA MACMU	PEPA_HUMAN	PEP2 MACFU		PEP1_MACFU
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735.5 32.9 386 1 PRPA PIG 735 32.8 387 1 PRPZ RABIT 717 32.0 387 1 PEPE RABIT 707.5 31.6 387 1 PEPE CHICK 708 31.4 387 1 PEPE CHICK 709 31.4 387 1 PEPE CALJA 700 31.3 396 1 CARP NEUCR 687.5 30.7 394 1 PEPE CAVPO 685 30.6 387 1 PEPE RABIT 680.5 30.4 392 1 PEPE RABIT 680.5 30.4 381 1 CHYM SHEEP
735.5 32.9 735 32.8 733 32.8 707.5 31.6 702 31.3 687.5 30.7 685 30.6 680.5 30.4 679.5 30.4
735.5 32.9 735 32.8 733 32.8 707.5 31.6 702 31.3 687.5 30.7 685 30.6 680.5 30.4 679.5 30.4
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ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       precursors.
-!- TISSUE SPECIFICITY: Expressed predominantly in adult lung (type II pneumocytes) and kidney and in fetal lung. Low levels in adult spleen and very low levels in peripheral blood Leukocytes.
-!- SIMILARITY: Belongs to peptidase family A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Bienkowski M.J., Shuck M.E., Slightom J.L., Drong R.F.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: May be involved in processing of pneumocyte surfactant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chunan Y., Bergman A.-C., Ueno T., Saito S., Sakaguchi K., Alaxya A.A., Franzen B., Bergman T., Arnott D., Auer G., Appella E., Joernvall H., Linder S., "Napsein A, a member of the aspartic protease family, is abundantly expressed in normal lung and kidney tissue and is expressed in lung
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. TISSUB-Kidney, and Lung; TISSUB-Kidney, and Lung; MEDLINE-9909289; Pubmed-9877162; Tatnell P.U., Powell D.U., Hill J., Smith T.S., Tew D.G., Kay J.; "Nappins: new human aspartic proteinases. Distinction between two
                                                                                                                                                                                             Homo sapiens (Human),
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Koelsch G., Wu S., Henthorn J., Tang J., Lin X., Koelsch G., Wu S., Henthorn J., Tang J., Lin X., "New human aspartic proteases napsin 1 and napsin 2: molecular cloning and intracellular localization of napsin 1."; Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                          (TA01/TA02)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND WASS SPECTROMETRY. TISSUE=Fetal lung; MEDLINE=20047840; PubMed=10580105;
                                                                          30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 41, Last annotation update)
Napsin l precursor (Rel. 3, 4.23.-) (Napsin A) (NAPA)
(Aspartyl protease 4) (Asp 4) (ASP4).
                                          420 AA
                                        PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                           closely related genes.";
FEBS Lett. 441:43-48(1998).
                                        STANDARD;
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SEQUENCE FROM N.A.
TISSUE=Liver;
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                                      NAP:1_HUMAN
096009:
RESULT 1
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musculus (Mouse)
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STRAIN=FVB/N; I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAIGGIPLLAGEYIILCSEIPKLPAVSFLLGGVWFNLTAHDYVIQTTRNGVRLCLSGFQA 360
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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15-JUL-1999 (Rel. 38, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Kidney-derived aspartic protease-like protein precursor (EC 3.4.23.-)
(KDAP-1) (KAP) (Napsin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MSPPPLLQPLLLLLPLLNVEPSGATLIRIPLHRVQPGRRILNLLRGWREPAELPKLGAPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGDKPIFVPLSNYRDVQYFGEIGLGTPPQNFTVAFDTGSSNLWVPSRRCHFFSVPCWLHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PGDKPIFVPLSNYRDVQYFGEIGLGTPPQNFTVAFDTGSSNLWVPSRRCHFFSVPCWLHH
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NAPSIN 1.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
M. O18B86AESBDOC865 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              99.7%; Score 2232; DB 1; Length 420; 99.8%; Pred. No. 2.7e-172;
                                                                                                                      MIM; 605631; -.
GO; GO:0004190; F:aspartic-type endopeptidase activity; TAS.
                                                                                                                                                                                                                                            Glycoprotein; Zymogen; Signal
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                                                                                                                                         GO; GO:0006508; P:proteolysis and peptidolysis; TAS. InterPro; IPR001969; Asprotease AS. InterPro; IPR009007; Pept A acid. InterPro; IPR001461; Peptidase A1. Pf00026; asp; 1.
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                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                       Pfam; PF00026; amp; 1.
PRINTS; PR00792; PEPSIN.
PROSTITE; PS00141; ASP PROTEASE; 2.
Hydrolase; Aspartyl protease; Glyc
                                        EMBL; AF090386; AAD04917.1; -.
EMBL; AF098484; AAD13215.1; -.
EMBL; AF200345; AAF17081.1; -.
HSSP; P00797; 2REN.
                                                                                                                                                                                                                                                                                                                                                                                                                     45386 MW;
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Matches 419; Conservative
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96
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354
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336 3
420 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-22388257; PubMed=1247932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altachus P. Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B. Duetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B. Duetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B. Duetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B.J., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B.J., Wann J., Wann J., Hsieh F.,

RA Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., McKwan P.J., WcKernan K.J., Malek J.A., Gunarathe P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

R. Mutting M. Acad. Sci. U.S.A. 99:16899-16903(2002).

T. TISSIE SPECIFICITY: Expressed at the highest levels in the kidney,

at a moderate level in the lung, and at low levels in the spleen

and adipose tissue.
                                                                                                                                                                              T., Muro S., Ozaki S.,
                                                                                                                                                                                                                                                                                                                                                                                        당
                                                                                                                                                                 Mori K., Ogawa Y., Tamura N., Ebihara K., Aoki T., Muro S., Ozaki S. Tanaka I., Tashiro K., Nakao K.; Molecular cloning of a novel mouse aspartic protease-like protein that is expressed abundantly in the kidney.";
                                                                                                                                                                                                                                                                                     [2]
SUGTENCE FROM N.A.
STRAIN=129/SvJ.
MEDLINE=20534768; PubMed=11082205;
Tathell P.J., Cook M., Peters C., Kay J.;
Molecular organization, expression and chromosomal localization the mouse pronapsin gene.";
Eur. J. Biochem. 267:6921-6930(2000).
                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mamnalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001969; Aspprotease_AS.
InterPro; IPR009007; Pept_A_acid.
InterPro; IPR001461; Peptidase_A1.
Pfam; PF00026; asp; 1.
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EMBL; AJ250719; CAB82907.1; JOINED.
EMBL; AJ250720; CAB82907.1; JOINED.
EMBL; BC014813; AAH14813.1; -.
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PROSITE; PS00141; ASP_PROTEASE; 2.
                                                                                                                   SEQUENCE FROM N.A.
STRAIN-BALB/c, TISSUE-Kidney;
MEDLINE-97165997; PubMed-9013890;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; D88899; BAA19004.1; -.
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VB/N; TISSUE=Kidney;
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MGD; MGI:109365; Kdap.
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                                                                        NCBI_TaxID=10090;
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Biol. 11:661-672(1992)
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HSSP; P07339; 1LYB.
MEROPS; A01.009; -.
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251
398 AA;
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                                                                                                                                                                                                                                                  243
                                                                                                                                                                                                                                                                                     DGILGLGREPTLAVGGVOPPLDAMVEQGLLEKPVFSFYLNRDSEGSDGGELVLGGSDPAHY 238
                                                                                                                                                                                                                                                                                                                       VPPLTFIPVTIPAYWQVHMESVKVGTGLSLCAQGCSAILDTGTSLITGPSEEIRALNKAI 298
                                                                                                                                                                                                                                                                                                                                                       PPPAGPFWILGDVFLGTYVAVFDRGDMKSSARVGLARARTRGADLGWGETAQAQF----P 419
                                                                                                                                                                                                                                                                                                            IPPLTFVPVTVPAYWQIHMERVKVGPGLTLCAKGCAAILDTGTSLITGPTEEIRALHAAI 303
                                                                                                                                                                                                                                                                                                                                             GGIPLLAGEYIILCSEIPKLPAVSFLLGGVWFNLTAHDYVIQTTRNGVRLCLSGFQALDV 363
                                                                                                                                                                                                        64 KPIFVPLSNYRDVQYFGEIGLGTPPQNFTVAFDTGSSNLWVPSRRCHFFSVPCWLHHRFD 123
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                  PKASSSFQANGTKFAIQYGTGRVDGILSEDKLTIGGIKGASVIFGEALWEPSLVFAFAHF
                                                                                                                                                                                                                                                                          DGILGLGFFILSVEGVRPPMDVLVEQGLLDKPVFSFYLNRDPEEPDGGELVLGGSDPAHY
                                                                                                                                                                       7 LOPLILLILPLL---NVEPSGATLIRIPLHRVQPGRRTLNLLRGWREPAELPKLGAPSPGD
                         KIDNEY-DERIVED ASPARTIC PROTEASE-LIKE
                                                                                    (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=F011icle;
MEDLINE=93039672; PubMed=1418623;
Retzek H., Steyrer E., Sanders E.J., Nimpf J., Schneider W.J.;
"Molecular cloning and functional characterization of chicken
                                                                                                                                                       <u>.</u>
و
                                                                                                                                       69.7%; Score 1560.5; DB 1; Length 419;
  Glycoprotein; Zymogen; Signal
                                                                                                                                                       Indels
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                                 PROTEIN.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC...) (COUNCED.
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                 ACTIVATION PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Cathopsin D precursor (EC 3.4.23.5).
Gallus gallus (Chicken).
                                                                                                               (GLCNAC
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37; Mismatches
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                                                                                                              N-LINKED
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                                                                                                                      45544 MW;
     protease;
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                                                                                                                                                        Conservative
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     Aspartyl
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     Hydrolase;
                                           ACT_SITE
ACT_SITE
DISULFID
DISULFID
DISULFID
                                                                                              CARBOHYD
                                                                                                               CARBOHYD
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          SIGNAL
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        165 VIEGEALWEPSLVEAFFAHFDGILGLGFPILSVEGVRPPMDVLVEQGILDKPVFSFYLNRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTSLITGPTEEIRALHAAIGGIPLLAGEYIILCSEIPKLPAVSFLLGGVWFNLTAHDYVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTAQPGGELLLGGTDPKYYSGDFSWVNVTRKAYWQVHMDSVDVANGLTLCKGGCBAIVDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Incerts, PF00026; asp; 1.
PRINTS; PR00792; PEPSIN.
PROSITE; PS00141; ASP_PROTEASE; 2.
PROSITE; PS00141; ASP_PROTEASE; 2.
1 MSPPPLLOPLLLILPLINVEPSGATLIRIPLHRVQPGRRTINLLRGWREPAELPKLGA--
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POTENTIAL.
CATHERSIN D.
BY SIMILARITY.
W.-LINKED (GLCNAC. . .) (POTENTIAL).
N.-LINKED (GLCNAC. . .) (POTENTIAL).
W., 584C99E2755AAZBI CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 46.0%; Score 1030; DB 1; Length 398; Local Similarity 50.0%; Pred. No. 1.5e-75; Alex 208; Conservative 57; Mismatches 115; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001969; Aspprotease AS.
InterPro; IPR009007; Pept A_acid.
InterPro; IPR001461; Peptidase_A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43298 MW;
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398
1157
96
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2283
1116
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133
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(Rel. 07, Created)
                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              precursor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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            Similarity
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Query Match
Best Local Simil
Matches 196; C
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10-OCT-2003
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SUBCELLULAR LOCATION: Lysosomal.

HISCELLANGOUS: The isoslectric point is 6.8. Has optimal activity at pH 2.5 with hemoglobin as the substrate and the optimal temperature is 37 degrees Celsius. This substrate and the optimal temperature is 37 degrees Celsius.

MINIARITY: Belongs to peptidase family Al.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO0792; PEPSIN.
PROSTIE; PSO0141; ASP PROTEASE; 2.
Hydrolase; Aspartyl protease; Glycoprotein; Lysosome; Signal; Zymogen.
SIGNAL
                                                                                                                                                                                                                                                                                                          TIŜSUE=Skeletal muscle;
MEDIINE=21165469; FubMed=11207447;
Nielsen L.B., Nielsen H.H.;
"Purification and characterization of cathepsin D from herring muscle
                                                                                                                                                                                                                                                                                                                                                                       Comp. Biochem. Physiol. 128B:351-363(2001).
-!- FUNCTION: Cathepsin D is an acid protease active in intracellular
  QTTRNGVRLCLSGFQALDVPPPAGPFWILGDVFLGTYVAVFDRGDMKSSARVGLAR 400
                Nielsen L.B., Stougaard P., Andersen P.S., Pedersen L.H.; "Cloning and sequence determination of herring muscle cathepsin D."; Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTIVATION PEPTIDE.
CATHERSIN D.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLUNAC. . .) (POTENTIAL).
MM; D0375DC38567A31B CRC64;
                                                                                                             28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-CCT-2003 (Rel. 42, Last amontation update)
Cathepsin D precursor (EC 3.4.23.5).
Clupea harengus (Alantic herring).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Clupeomorpha; Clupeidae;
                                                                                                                                                                                                                                                                                                                                                                                                                        in
                                                                                                                                                                                                                                                                                                                                                                                              protein breakdown. CATALYTIC ACTIVITY: Specificity similar to, but narrower that of pepsin A. Does not cleave the 4-Gln-[-His-5 bond chain of insulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- ENZYME REGULATION: Inhibited by pepstatin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEROPS; A01.009; -.
InterPro; IPR001969; Aspprotease AS.
InterPro; IPR001907; Pept A_acid.
InterPro; IPR001461; Peptidase_A1.
Pfam; PF00026; asp; 1.
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                                                                                       STANDARD;
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396
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396 AA;
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                                                                                                                                                                                                                                                                                                                                                             (Clupea harengus)."
                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                  Clupea.
NCBI_TaxID=7950;
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ACT_SITE
DISULFID
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374
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                                                                                                                                                                                                                                         TKFALQYGTGRVDGILSEDKLTIGGIKGASVIFGEALWEPSLVFAFFAHFDGILGLGFPIL 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SVEGVRPPMDVLVEQGLLDKPVFSFYLNRDPREPDGGELVLGGSDPAHYIPPLTFVPVTV 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAYWQIHMERVKVGPGLTLCAKGCAAILDTGTSLITGPTEEIRALHAAIGGIPLLAGEYI 314
                                                                                                        74
                                                                                                                                       26 LIRIPLHRVQPGRRTLN-----LLRG---WREPAELDKLGAPSPGDKPIFVPLSNYR
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MELLINE=87231068; PubMed=3588310;
WestLiay B.R., May F.B.B.;
Wostrogen regulates cathepsin D mRNA levels in oestrogen responsive human breast cancer cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Kidney,
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nomo saprota; Metarcas; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metheria; Primates; Catarrhini; Hominidae; Homo.
Mammalia; Eutheria; Primates;
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MEDILINE=91299158; PubMed=2069717;
Redecker B., Heckendorf B., Grosch H.W., Mersmann G., Hasilik .
Molecular organization of the human cathepsin D gene.";
DNA. Cell Biol. 10:423-431(1991).
  DB 1; Length 396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIINE-85270436; PubMed-3927292;
Faust P.L., Kornfeld S., Chirgwin U.M.;
"Cloning and sequence analysis of cDNA for human cathepsin
Proc. Natl. Acad. Sci. U.S.A. 82:4910-4914(1985).
                                               Indels
                         pred. No. 1.1e-74;
62; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
(EC 3.4.23.5).
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45.6%; Score 1019.5; 50.6%; Pred. No. 1.1e
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Nucleic Acids Res. 15:3773-3786(1987).
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Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Ioquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

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Richards S., Worley K.C., Sodergren B.J., Lu X., Gibbs R.A.,

Rahesley J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Milialon D.K., Muny D.W., Green B.D., Dickson M.C.,

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-!-FUNCTION: Acid protease active in intracellular protein breakdown.
- Involved in the pathogenesis of several diseases such as breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22660472; PubMed=12754519; Zhang H., Li X.-J., Martin D.B., Abbersold R.; Zhang H., Li X.-J., Martin D.B., Abbersold R.; Ilderfication and quantification of N-linked glycoproteins using hydrazide chemistry, stable isotope labeling and mass spectrometry."; Nat. Biotechnol. 21:660-666(2003).
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"Two crystal atructures for cathepsin D: the lysosomal targeting
signal and active site.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                               "Characterization of the proximal estrogen-responsive element of human cathepsin D gene.";
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MEDLINE=95021301; PubMed=7935485;
Augereau P., Miralles F., Cavailles V., Gaudelet C., Parker M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANT VAL-58.
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Papassociropoulos A., Bagli M., Kurz A., Kornhuber J., Forstl F Papassociropoulos A., Lautenschlager N., Heun R.;
Maier W., Pauls J., Lautenschlager N., Heun R.;
"A genetic variation of cathepsin D is a major risk factor for Alzheimer's disease.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mol. Endocrinol. 8:693-703(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ann. Neurol. 47:399-403 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 170-180.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Rochefort H.;
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N-LINKED (GLCNAC. ..).
A -> V (ASSOCIATED WITH INCREASED RISK IN AD; POSSIBLY INFLUENCES SECRETION AND INTRACELLULAR MATURATION; dbSNP:17571).
/FIId=VAR_011621.
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InterPro; IPR001969; Aspprotease AS.
InterPro; IPR00161; Peptidase Al.
Pfan; PF00026, asp; l.
PROSTIE; PS00141; ASP PROTEASE; 2.
PROSTIE; PS00141; ASP PROTEASE; 3.
PROSTIE: ASP PROTEASE; 3.
PROSTIE: ASP PROTEASE; 3.
PROSTIE: ASP PROSTIE: 
             -1- CATALYTIC ACTIVITY: Specificity similar to, but narrower than, that of pepain A. Does not cleave the 4-Gln-|-His-5 bond in B chain of insulin.
-1- SUBUNIT: Consists of a light chain and a heavy chain.
-1- SUBCHILLAR LOCATION: Lysosomal.
-1- BOLYMORPHISM: The Val-58 allele is significantly overrepresented in demented patients (11.8%) compared with nondemented controls (4.9%). Carriers of the Val-58 allele have a 3.1-fold increased risk for developing AD than noncarriers.
-1- SIMILARITY: Belongs to peptidase family Al.
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CATHERSIN D.
CATHERSIN D.
CATHERSIN D. LICHT CHAIN (PROBABLE)
CATHERSIN D. LEAVY CHAIN (PROBABLE)
cancer and possibly Alzheimer's disease. CATALYTIC ACTIVITY: Specificity similar
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EMBL; M63144; CAA28955.1; --
EMBL; M631348; AAA51922.1; --
EMBL; M63135; AAA51922.1; JOINED.
EMBL; M63135; AAA51922.1; JOINED.
EMBL; M63136; AAA51922.1; JOINED.
EMBL; M63136; AAA51922.1; JOINED.
EMBL; M63136; AAA51922.1; JOINED.
EMBL; BC016320; AAH16320.1; --
EMBL; S2567; AAA13868.1; --
EMBL; S2557; KHHUD.
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Siera-2DPAGE; P07339; -.
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MIM; 116840; -
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1LYB; 31-JAN-94.
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MEROPS; A01.009; -.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCSI TaxID=10116;
                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                          DB 1; Length 412;
                                                                                                                                                                                                                                                        45.4%; Score 1015; DB 1; Length 4 46.9%; Pred. No. 2.6e-74; rive 71; Mismatches 125; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
08-EFB-2003 (Rel. 41, Last annotation update)
Cathepsin D precursor (EC 3.4.23.5).
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Best Local Similarity 46.9
Matches 196; Conservative
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-!- SUBUNIT: Occurs as a mixture of both a single chain form and two subunit: Occurs as a mixture of both a single chain form and types of two chain (light and heavy) forms.
-!- SUBCELUMAR LOCATION: Lysoscomal.
-!- SIMILARITY: Belongs to peptidase family Al.
                                        Fujita H., Tanaka Y., Noguchi Y., Kono A., Himeno M., Kato K., "Isclation and sequencing of a cDNA clone encoding rat liver lyscsomal cathepsin D and the structure of three forms of mature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68; Mismatches 124; Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 134-170.
MEDLINE=89034127; PubMed=3182800;
Yonezawa S., Takahashi T., Wang X., Wong R.N.S., Hartsuck J.A.,
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CATHEREIN D.
CATHEREIN D. AD LIGHT CHAIN.
CATHEREIN D 30 KDa HERNY CHAIN.
CATHEREIN D 34 KDa HERNY CHAIN.
CATHEREIN D 34 KDa HERNY CHAIN.
CATHEREIN D 34 KDA HERNY CHAIN.
BY SIMILARITY.
BY 
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InterPro; IPR001969; Pept A_acid.
InterPro; IPR001461; Pept A_acid.
InterPro; IPR001461; Peptidase_A1.
Permir PF00026; asp; 1.
PRINTS; PR00792; asp; 1.
PROSITE; PS00141; ASP PROTEASE; 2.
Hydrolase; Aspartyl protease; Glycoprotein; Zymogen; Signal;
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163 D -> T (IN REF. 3).
205 K -> N (IN REF. 2).
262 K -> N (IN REF. 2).
44680 MW; C423AD4104D95F84 CRC64;
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48.3%; Pred. No. 1.6e-73;
                                                                                                                                                                                                                                                                       Biochem. Biophys. Res. Commun. 179:190-196(1991)
MEDLINE=91354249; PubMed=1883350;
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DISULFID
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SEQUENCE FROM N.A.

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SEQUENCE FROM N.A.

STRAIN=C57BL/6J; TISSUE=Brain, and Mammary gland;

MEDIINE—238825; PubMed=12477932;

ALESTAIN FOR T., Feingold E.A., Grouse L.H., Derge J.G.,

ALESCALI S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Habeh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

R Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

R Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
                                                                                      237
                                                                                                              244
SDPAHYIPPLIFVPVTVPAYWQIHMERVKVGPGITLCAKGCAAILDIGTSLITGPTEEIR 297
                                                                                                                                                  ALHAAIGGIPLLAGEYIILCSEIPKLPAVSFLLGGVWFNLTAHDYVIQTTRNGVRLCLSG 357
                                                   SDKSBIYVKNGTSFDIHYGSGSLSGYLSQDIVSVPCKSDLGGIKVEKQIFGEATKQPGVV
                                                                                                305 ELQKAIGAVPLIQGEYMIPCEKVSSLPIITFKLGGQNYELHPEKYILKVSQAGKTICLSG
                                      ----KLTIGGIKGASVIFGEALWEPSLV
                                                                                    FAFAHFDGILGLGFPILSVEGVRPPMDVLVEQGLLDKPVFSFYLNRDPEEPDGGELVLGG
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DNA Cell Biol. 13:419-427(1994).
                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6J; TISSUE=Brain;
MEDLINE=91088345; PubMed=2263503;
Diedrich J.F., Staskus K.A., Retzel E.F., Haase A.T.;
"Nucleotide sequence of a cDNA encoding mouse cathepsin D.";
Nucleic Acids Res. 18:7184-7184(1990).
                                                                                                                                                                                                                               FQALDVPPPAGPFWILGDVFLGTYVAVFDRGDMKSSARVGLARART 403
                                                                                                                                                                                                                                            365 FMGMDIPPPSGPLWILGDVFIGCYYTVFDR----EYNRVGFAKAAT 406
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(Rel. 16, Last sequence update)
(Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=90326544; PubMed=2374732;
MEDLINESPY M.J., Mitchell S.C., Glimcher L.H.;
"Molecular cloning of mouse cathepsin D.";
Nucleic Acids Res. 18:4008-4008(1990).
                                     124 PKASSSFQANGTKFALQYGTGRVDGILSED-
                                                                                                                                                                                                                                                                                                                                                                          Cathepsin D precursor (EC 3.4.23.5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6J;
MEDLINE=94280622; PubMed=8011168;
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EPVSELLKNYLDAQYYGDIGIGTPPQCFTVVFDTGSSNLWVPSIHCKILDIACWVHHKYN 124
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Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green El.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Smailus D.E., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
-!- FUNCTION: Acid procease active in intracellular protein breakdown. -!- CATALYTIC ACTIVITY: Specificity similar to, but narrower than, that of peopsin A. Does not cleave the 4-Gln-[-His-5 bond in B.
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CATHEPSIN D.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (BY SIMILARITY).
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PROSITE; PS00141; ASP_PROTEASE; 2.
Hydrolase; Aspartyl protease; Glycoprotein; Lysosome; Zymogen;
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                                                                                                                                                                                                                                                                                                                                                               chain of insulin.
--- SUBUNIT: Consists of a light chain and a heavy chain.
--- SUBCELIULAR LOCATION: Lysosomal.
--- SIMILARITY: Belongs to peptidase family Al.
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InterPro; IPR009007; Pept A acid.
InterPro; IPR001461; Peptidase_A1.
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EMBL; X68378; CAA48453.1; -.
EMBL; X68378; CAA48453.1; JOINED.
EMBL; X68380; CAA48453.1; JOINED.
EMBL; X68381; CAA48453.1; JOINED.
EMBL; X68381; CAA48453.1; JOINED.
EMBL; X68382; CAA48453.1; JOINED.
EMBL; BCO57931; AA454788.1; -.
EMBL; BCO57931; AA454788.1; -.
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MGD; MGI:88562; Ctsd.
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261
410 AA;
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HSSP; P07339; 1LYB.
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                                                                                               125 SDKSSTYVKNGTSFDIHYGSGSLSGYLSQDTVSVPCKSDQSKARGIKVEKQIFGEATKQP 184
                                                                                     EIRALHAAIGGIPLLAGEYIILCSEIPKLPAVSFLLGGVWFNLTAHDYVIQTTRNGVRLC 354
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                                                   235 LGGSDPAHYIPPLTFVPVTVPAYWQIHMERVKVGPGLTLCAKGCAAILDTGTSLITGPTE
                                                                                                                                                                                                                                             Bos taurus (Bovine).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                                                                                                           Larsen L.B., Boisen A., Petersen T.B.;
"Procathepsin D cannot autoactivate to cathepsin D at acid pH.";
FEBS Lett. 319:54-58(1993).
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Pfam; PF00026; asp; 1.
PROSTE; PR00141; ASP_PROTEASE; 2.
Hydrolase; Aspartyl protease; Glycoprotein; Lysosome; Zymogen.
Hydrolase; Aspartyl protease; Glycoprotein; Lysosome; Zymogen.
                                                                                                                               365 LSGFMGMDIPPPSGPLWILGDVFIGSYYTVFDR----DNNRVGFANA 407
                                                                                                                        LSGFQALDVPPPAGPFWILGDVFLGTYVAVFDRGDMKSSARVGLARA 401
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 45-390, AND X-RAY CRYSTALLOGRAPHY (3 ANGSTROMS) TISSUE-Liver:
                                                                                                                                                                                                   01-JUL-1993 (Rel. 26, Created)
16-007-2001 (Rel. 40, Last sequence update)
18-EFB-2003 (Rel. 41, Last annotation update)
Cathepsin D precursor (EC 3.4.23.5).
                                                                                                                                                                                    390 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001969; Aspprotease AS.
InterPro; IPR009007; Pept A acid.
InterPro; IPR001461; Peptidase_A1.
                                                                                                                                                                                                                                                                                                                   MEDLINE=93202276; PubMed=8454061;
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                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                       Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
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MEROPS; A01.009; -.
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DISULFID
CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 NVTRQAYWQIHWDQLDVGSSLTVCKGGCEAIVDTGTSLIVGPVEEVRELQKAIGAVPLIQ 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PVTVPAYWQIHMERVKVGPGLTLCAKGCAAILDTGTSLITGPTEEIRALHAAIGGIPLLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GEYIILCSEIPKLPAVSFLLGGVWFNLTAHDYVIQTTRNGVRLCLSGFQALDVPPPAGPF
                                                                                                                                                                                                                                                                                                                                                                                         26 LIRIPLHRVQPGRRTLNLLRGW-----REPAELPKLGAPSPGDKPIFVPLSNYRDVQYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 VIRIPLHKFTSIRRTMSEAAGXVXXLIAKGPISKYATGEPAVRQGPIPELLKNYMDAQYY
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                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cho W.-L., Dhadialla T.S., Raikhel A.S.;
"Purification and characterization of a lysosomal aspartic protease
with cathepsin D activity from the mosquito.";
Insect Biochem. 21:165-176(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cloning of cDNA for mosquito lysosomal aspartic protease. Sequence analysis of an insect lysosomal enzyme similar to cathepsins D and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last sequence update)
128-72B-21003 (Rel. 41, Last annotation update)
128-72B-2103 (Rel. 41, Last annotation update)
128-72B-2103 (Rel. 41, Last annotation update)
128-2103 (Rel. 41, Last annotation update)
128-2103 (Rel. 41, Last annotation)
128-2103 (Rel.
                                                                                                                                                                                                                                                                               19;
                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                               58; Mismatches 125; Indels
241 N-LINKED (GLCNAC. . .) 'F' 42488 MW; 5B38AAIC33C48D35 CRC64;
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-1- SUBCELLULAR LOCATION: Lysosomal.
-1- SIMILARITY: Belongs to peptidase family Al.
                                                                                                                                                               Score 967.5; DB Pred. No. 1.6e-70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WILGDVFLGTYVAVFDRGDMKSSARVGLARA 401
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MEDLINE=93016141; Pubmed=1400492;
Cho W.L., Raikhel A.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biol. Chem. 267:21823-21829(1992).
                                                                                                                                                                                                                    48.3%;
                                                                                                                                                                                                                                                                               Matches 189; Conservative
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                                               390 AA;
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Local Simi
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CAREOHYD
VARIANT
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                             66 IFVPLSNYRDVQYFGEIGLGTPPQNFTVAFDTGSSNLWVPSRRCHFFSVPCWLHHRFDPK 125
                                                                                                                                                                                                                                                                                                                       SG VPEPLSNYLDAQYYGAITIGTPPQSFKVVFDTGSSNLWVPSKECSFTNIACLMHNKYNAK 115
                                                                                                                                                                                                                                                                                                                                                 126 ASSSFQANGTKFALQYGTGRVDGILSEDKLTIGGIKGASVIFGEALWEPSLVFAFAHFDG 185
                                                                                                                                                                                                                                                                                                                                                                                               246 PLIFVPVTVPAYWOIHMERVKVGPGLTLCAKGCAAILDTGTSLITGPTEEIRALHAAIGG 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                          306 IPLLAGEYIILCSEIPKLPAVSFLLGGVWFNLTAHDYVIQTTRNGVRLCLSGFQALDVPP 365
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                                                                                                                                                                                                                                                                                    6 ILOPILILIIPULNVEPSGATLIRIPLHRVQPGRRTINLLRGWREPAELPKLGAPSPGDKP
                                                                                                                                                                                                                                                         11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sus scrofa (Pig).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Butheria, Cetartiodactyla, Suina, Suidae; Sus.
NCBL_TaxID=9823;
                                 PIR; A45117; A45117.

MEXOPS: 2REN.

MEXOPS: 2REN.

MEXOPS: 2.2PAGE; Q03168; -.

Siena-2DPAGE; Q03168; -.

InterPro; IPR001969; Aspprotease_AS.

InterPro; IPR001969; Pept A acid.

InterPro; IPR001461; Peptidase_A1.

Pfam; PF00126; asp; 1.

PRINTS; PR00792; PEPSIN.

PROSITE; PS00141; ASP_PROTEASE; 2.

Hydrolase; Aspartyl 18
                                                                                                                                                                                                             .) (POTENTIAL)
                                                                                                                                                                                                                                        DB 1; Length 387;
                                                                                                                                                     LYSOSOWAL ASPARTIC PROTEASE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
NY SIMILARITY.
N SIMILARITY.
N-LINKED (GLCNAC. ..) (POTEN
                                                                                                                                                                                                                                      ; Score 964.5; DB 1; Length 3; Pred. No. 2.8e-70; 62; Mismatches 131; Indel8
                                                                                                                                                                                                                -LINKED (GLCNAC. . .) (Po
73A3C9E701E47EEC CRC64;
                                                                                                                                              REMOVED IN MATURE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              366 PAGPFWILGDVFLGTYVAVFDRGDMKSSARVGLARA 401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
PERB-2003 (Rel. 41, Last annotation update)
Cathepsin D (EC 3.4.23.5).
                                                                                                                                                                                                                      41805 MW;
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                         EMBL; M95187; AAA29350.1;
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387
272
106
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343
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123
387 AA;
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ACT_SITE
DISULFID
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CARBOHYD
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Best Local
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65 PIFVPLSNYRDVQYFGEIGLGTPPQNFTVAFDTGSSNLWVPSRRCHFFSVPCWLHHRFDP 124
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                                    Takahashi T., Tang J.;
"Amino acid sequence of porcine spleen cathepsin D light chain.";
J. Biol. Chem. 258:6435-6443(1983).
                                                                                                                                                                                                                                       SEQUENCE OF 74-148 FROM N.A.
MEDLINE=89034127; PubMed=3182800;
Yonezawa S., Takahashi T., Wang X., Wong R.N.S., Hartsuck J.A.,
                                                                                                                                                                                                                                                                                                                  "Structures at the proteolytic processing region of cathepsin J. Biol. Chem. 263:16504-16511(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zymogen.
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G -> Q.

MISSING (IN REF. 1).

C -> S (IN REF. 1).

W; B3E72C11787F14E2 CRC64;
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PRINTS; PR00141; ASP_PROTEASB; 2.
PROSITE; PS00141; ASP_PROTEASB; 2.
Hydrolase; Aspartyl protease; CATHEPSIN D HIGHT CHAIN.
                                                                                                                                                                                       D.";
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                                                                                                                                                                 Shewale J.G., Tang J.;
"Amino acid sequence of porcine spleen cathepsin
Proc. Natl. Acad. Sci. U.S.A. 81:3703-3707(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (
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InterPro; IPR009007; Pept A acid.
InterPro; IPR001461; PeptIdase_A1.
Pfam; PP00026; asp; 1.
TISSUE=Spleen;
MEDLINE=83213348; PubMed=6406481;
                                                                                                                             TISSUE=Spleen;
MEDLINE=84222027; PubMed=6587385;
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37295 MW;
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                                                                                                           SEQUENCE OF 104-345.
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97
345 AA;
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Aspartyl
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01-NOV-1997 (Re]
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72
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365
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             Lysosome, I
NON TER
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CHAIN
ACT SITE
ACT SITE
  Hydrolase;
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                                                                                           DISULFID
DISULFID
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SEQUENCE
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CATE_MOUSE
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CATALYTIC ACTIVITY: Specificity similar to, but narrower than, protein Deakdown.

CHALYTIC ACTIVITY: Specificity similar to, but narrower than, that of pepsin A. Does not cleave the 4-Gln-[-His-5 bond in B chain of insulin.

CHECKLOWER: Description A. Does not cleave the a single chain form and two types of two chain (light and heavy) forms (By similarity).

CHECKLOWER: Defects in CTSD are a cause of congenital ovine neuronal ceroid lipofuscinosis (CONCL). CONCL is an autosomal recessive disorder. Newborn lambs are week, trempling, and unable to rise and support their bodies. However, they are able to vocalize, support their heads, and to suckle if bottle-fed. At autopsy, the brains of affected lambs are strikingly small. The deep layers of the cerebral cortex show pronounced neuronal loss, reactive astrocytosis, and infiltration of macrophages. There is severe degeneration of hippocampal pyramidal neurons.

CHECKLOWER: Deach of the procampal pyramidal neurons.

CHECKLOWER: Deach of the procampal pyramidal neurons.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                242 EVRELGKAIGAVPLIQGEYMIPCEKVPSLPDVTVTLGGKKYKLSSENYTLKVSQAGQTIC 301
                                                                                                                                                                                                                                                                                                                                                                                                                                              ., Sleat D.E., Gin R.M., Donnelly R.J., Baumann M.,
                             LGGSDPAHYIPPLTFVPVTVPAYWQIHMERVKVGPGLTLCAKGCAAILDTGTSLITGPTE
                                                                    EIRALHAAIGGIPLLAGEYIILCSEIPKLPAVSFLLGGVWFNLTAHDYVIQTTRNGVRLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- FUNCTION: Cathepsin D is an acid protease active in intracellular
                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "A mutation in the ovine cathepsin D gene causes a congenital lysosomal storage disease with profound neurodegeneration."; EMBO J. 19:2786-2792(2000).
                                                                                                                                          LSGFQALDVPPPAGPFWILGDVFLGTYVAVFDRGDMKSSARVGLARA 401
                                                                                                                                                                                                                                                  (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
precursor (EC 3.4.23.5) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND VARIANT CONCL ASN-268
                                                                                                                                                                                                                         365 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nterPro; IPR001969; Aspproteage AS.
InterPro; IPR009007; Pept A acid.
InterPro; IPR001461; Peptidase_A1.
                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=White Swedish Landrace;
MEDLINE=201315862; PubMed=10856224;
TYYDRELA J., Sohar I., Sleat D.E., (Haltia M., Lobel P.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00026; asp; 1.
PRINTS; PR00792; PEPSIN.
PROSITE; PS00141; ASP_PROTEASE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF164143; AAF80494.1; -.
HSSP; P07339; 1LYB.
                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                            Cathepsin D precursor
                                                                                                                                                                                                                                                                                                                        Ovis aries (Sheep)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P07339; 1L
MEROPS; A01.009;
                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9940;
                                                                                                                                                                                                                                                     16-0CT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58 iGIGTPPQCFTVVPDTGSANLWVPSIHCKLLDIACWVHHKYNSDKSSTYVKNGTTFDIHY 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TVPAYWQIHMERVKVGPGLILCAKGCAAILDIGISLITGPIEEIRALHAAIGGIPLLAGE 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YIILCSEIPKLPAVSFLLGGVWFNLTAHDYVIQTTRNGVRLCLSGFQALDVPPPAGPFWI 372
                                                                                                                                                                                                                                                                                                                                                                                                                                         57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82 IGLGTPPQNFTVAFDTGSSNLWVPSRRCHFFSVPCWLHHRFDPKASSSFQANGTKFAIQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       142 GTGRVDGILSEDKLTI-----GGIKGASVIFGEALWEPSLVFAFAHFDGILGLGFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ILSVEGVRPPMDVLVEQGLLDKPVFSPYLNRDPEEPDGGELVLGGSDPAHXIPPLTFVPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   178 RISVNNVLPVFDNLMRQKLVDKAVFSFFLNRDPKAQPGEELMLGGTDSKYYRGSLTYHNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tatnell P.J., Lees W.E., Kay J.; "Cloning, expression and characterisation of murine procathepsin E."; FEBS Lett. 408:62-66(1997).
                                                                                                                                                                                                                                                                                                                                                                                                 31 LHRVQPGRRTLNLLRGWREPAE-----LPKLGAPSPGDK--PIFVPLSNYRDVQYFGE
                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                          21;
                                                                                                                                                                                                                                                                                                                  41.2%; Score 922.5; DB 1; Length 365; 47.7%; Pred. No. 6.2e-67;
                                                         ACTIVATION PEPTIDE.
CATHEFSIN D.
BY SIMILARITY.
CONCL; INACTIVE).
                                                                                                                                                                                                                                                                                                                                                          Indels
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STRAND=129/SvJ;
Tatnell P.J., Roth W., Duessing J., Kay J., Peters C.;
Sutmitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                        39814 MW; 76A7BFE5BC45E9CB CRC64;
protease; Glycoprotein; Zymogen;
                                                                                                                                                                                                                                                                                                                                    Pred. No. 6.2e-67;
61; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Cathepsin E precursor (EC 3.4.23.34).
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STRAIN-BALB/C; TISSUE-Spleen;
MEDLINE-97324100; Pubmed-9180269;
                          Disease mutation.
                                                                                                                                                                                                                                                                                                                                                              fatches 175; Conservative
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                                                               265
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CATE HUMAN
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                                                                                                      KA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

KAusner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Antschul S.F., Jeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Antschul S.F., Jozdan H., Moore T., Max S.I., Wang J., Hsieh F.,

Blatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong I.,

Batchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong I.,

Brownstein M.J., Ugdin T.B., Toshlyuki S., Carninci P., Prange C.,

Raba S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gullar R.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,

Allalon D.K., Muxry D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Allalon D.K., Muxry D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Antilaton D.K., Muxry D.W., Sodergren E.J., Lu X., Gibbs R.A.,

Antilaton D.K., Muxry D.W., Sodergren E.J., Lu X., Gibbs R.A.,

Rabes J. G., Grimwood J., Schwutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Schnerch A., Schehul J.E., Jones S.J.W., Marra M.A.,

R. Generation and initial analysis of more than 15,000 full-length

Human and mouse cDNA sequences.

Froc. Natl. Acad. Sci. U.S.A., 99:16899-16030[2002].

Froc. Natl. Acad. Sci. U.S.A., 99:16899-16030[2002].

Iymphoid associated tissue, it may have a role in immune function.

Iymphoid associated tissue, it may have a role in immune function.

Inmphoid associated tissue, it may have a role in immune function.

Incorrections and interpretation and distribution in Ispander and Absociated tissue, it may have a role in immune function.

Incorrections and interpretation and distribution in Ispander and Sci. U.S.A., 99:16899-16899-1690 and distribution.
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ACTIVATION PEPTIDE (BY SIMILARITY).

CATHERSIN E.

BY SIMILARITY.

INTERCHAIN (PROBABLE).

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. ..) (POTENTIAL).

N-LINKED (GLCNAC. ..) (POTENTIAL).

H -> Q (IN REF. 2).
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PROSITE; PRO0792; PEPSIN

PROSITE; PS00141; ASP_PROTEASE; 2.

Hydrolase; Aspartyl protease; Glycoprotein; Zymogen; Signal.

PROPEP 19 Armitmarks name of the property 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: Homodimer; disulfide-linked (By similarity). SIMILARITY: Belongs to peptidase family Al.
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42932 MW; 83993FFE3AB36105 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39.2%; Score 878; DB 1; 45.5%; Pred. No. 2.6e-63;
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InterPro; IPR009007; Pept A acid.
InterPro; IPR001461; Peptidase_A1.
                  SEQUENCE FROM N.A.
STRAIN-FVB/N; TISSUE=Mammary gland;
MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X97399; CAA66056.1; -.
EMBL; Y10928; CAA71859.1; -.
EMBL; BC005432; AAH05432.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               397
97
282
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323
297
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323
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397 AA;
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ACT_SITE
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DISULFID
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14;

67; Mismatches 138; Indels

Conservative

183;

Matches

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238
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                                                                                                                                                                                                                                                                                                                                                   300 HAAIGGIPLLAGEYIILCSEIPKLPAVSFLLGGVWFNLTAHDYVIQTTRNGVRLCLSGFQ 359
SPGDKPIFVPLSNYRDVQYFGEIGLGTPPQNFTVAFDTGSSNLWVPSRRCHFFSVPCWLH
                       CNVYSSVNEPLINYLDMEYFGTISIGTPPQNFTVIFDTGSSNLWVPSVYC--TSPACKAH
                                                                                       HRFDPKASSSFQANGTKFAIQYGTGRVDGILSEDKLTIGGIKGASVIFGKALWEPSLVFA
                                                                                                              119 PVFHPSQSDTYTEVGNHFSIQYGTGSLTGIIGADQVSVEGLTVDGQQFGSSVKEPGQTFV
                                                                                                                                                                                                      179 NAEFDGILGLGYESLAAGGVTPVFDNMMAQNLVALPMFSVYLSSDPQGGSGSELTFGGYD
                                                                                                                                                                                                                                                                                            180 FAHFDGILGLGFPILSVEGVRPPMDVLVEQGLLDKPVFSFYLNRDPEEPDGGELVLGGSD
                                                                                                                                                                                                                                                                PAHYIPPLIFVPVTVPAYWQIHWERVKVGPGLTLCAKGCAAILDTGTSLITGPTEEIRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Brain;
MEDILINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
HOpkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hashe F.,
Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Garninci P., Prange C.,
Brownstein M.J., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Rosex S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIME=92112877; PubMed=1370478;
Azuma T., Liu W.G., Vander Laan D.J., Bowcock A.M., Taggart R.T.;
"Human gastric cathepsin E gene. Multiple transcripts result from
"Hernative polyadenylation of the primary transcripts of a single
gene. locus at 1q31-q32.";
J. Hiol. Chem. 267:1609-1614(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIANE=89380302; PubMed=2674141;
Azuma T., Pals G., Mohandas T.K., Couvreur J.M., Taggart R.T.;
"Human gastric cathepsin E. Predicted sequence, localization to
chromosome 1, and sequence homology with other aspartic
proteinases.";
J. Biol. Chem. 264:16748-16753 (1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    360 ALDVPPPAGPFWILGDVFLGTYVAVFDRGDMKSSARVGLARA 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01.JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-CCT-2003 (Rel. 42, Last annotation update)
Cathepsin E precursor (EC 3.4.23.34).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      396 A.A.
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Tatnell P.J., Kay J.,
"HUman procathepsin E.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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Name=Long;
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                                                                                                                                                         SEQUENCE OF 54-68; 77-95; 141-155; 275-285 AND 389-396.
MEDLINE=90241267; PubMed=2334440;
Athauda S.B.P. Matsuzaki O., Kgeyama T., Takahashi K.;
Athauda S.B.P. Matsuzaki O., Kgeyama T., Takahashi K.;
Structural evidence for two isozymic forms and the carbohydrate attachment site of human gastric cathepsin E.";
Biochem. Biophys. Res. Commun. 168:878-885(1990).
-!- FUNCTION: Due ot its intracellular location and distribution in lymphoid associated tissue, it may have a role in immune function.
-!- CATALYTIC ACTIVITY: Similar to cathepsin D, but slightly broader
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman U.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIM, 116890, -.

MIM, 116890, -.

InterPro; IPR001969; Aspprocease AS.

InterPro; IPR001961; Pept A acid.

InterPro; IPR001961; Pept A acid.

InterPro; IPR001961; Pept A acid.

Fram; PR00105; asp; 1.

PRINTS; PR00792; PEPSIN.

PROSITE; PS00141; ASP PROTEASE; 2.

Hydrolase; Aspartyl protease; Glycoprotein; Zymogen; Signal; Polymorphism; Pyrrolidone carboxylic acid; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /FTId=VAR 014572.
40B643C5FB01521E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATHEPEIN E.
PYRROLIDONE CARBOXYLIC AC
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (PROBABLE).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
O-LINKED (GLCNAC. ..).
O-LINKED (POTENTIAL).
C-LINKED (POTENTIAL).
T-> I (in dbSNP:6503).
                                                                                                                  human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACTIVATION PEPTIDE
                                                                                                                                                                                                                                                                                                        SÜBUNIT: Hömodimer; disulfide-linked. SIMILARITY: Belongs to peptidase family Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ), M84424, AAA52300.1; -
), M64413, AAA52300.1; JOINED.
), M84418, AAA52300.1; JOINED.
), M84419; AAA52300.1; JOINED.
), M84419; AAA52300.1; JOINED.
), M84421; AAA52300.1; JOINED.
), M84421; AAA52300.1; JOINED.
), M84422; AAA52300.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J05036; AAA52130.1; -.
AJ250717; CAB82850.1; -.
BC042537; AAH42537.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42793 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A42038; A34401.
PDB; 1LCG; 17-APR-02.
MEROPS; A01.010; --
Genew; HGNC:2530; CTSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60
1114
276
351
90
2220
333
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396
18
96
281
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                                                                                                                                                                                                                                                                                              specificity.
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ACT_SITE
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CHAIN
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EMBL;
EMBL;
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EMBL;
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                                                                                                                                                                                                                                                      | : || | : | : | : | | : | | : | | 303 AAP-VDGEYAVECANLNVMPDVTFTINGVPYTLSPTAXTILDFVDGMQFCSSGFQGLDIH 361
                                                                                                                                                                                                                                                                                                          GILGLGFPILSVEGVRPPMDVLVEQGLLDKPVFSFYLNRDPERPDGGELVLGGSDPAHYI 244
                                                                                                                                                                                                                                                                                                                                                                                         245 PPLTFVPVTVPAYWQIHMERVKVGPGLTLCAKGCAAILDTGTSLITGPTEEIRALHAAIG 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GIPLLAGEYIILCSEIPKLPAVSFLLGGVWFNLTAHDYVIQTTRNGVRLCLSGFQALDVP 364
                                                                                                                                                      65 PIFVPLSNYRDVQYFGEIGLGTPPQNFTVAFDTGSSNLWVPSRRCHFFSVPCWLHHRFDP 124
                                                                                                                    64
                                                                                                      125 KASSSFQANGTKFAIQYGTGRVDGILSEDKLTIGGIKGASVIFGEALWEPSLVFAFAHFD
                                                                            LLLLLPLLNVEPSGATLIRIPLHRVQPGRRTL----NLLRGWR-EPABLPKLGAPSPGDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQTENCE OF 59-110.
MEDLINE=90147750; PubMed=2105725;
Yonezawa S., Takahashi T., Ichinose M., Miki K., Tanaka J., Gasa S.;
Yonezawa S., Takahashi T., Ichinose M., Miki K., Tanaka J., Gasa S.;
Yonezawa S., Takahashi T., Ichinose M., Miki K., Tanaka J., Gasa S.;
Yonezawa S., Tatakahashi E. amino-terminal structure and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Okamoto K., Yu H., Misumi Y., Ikehara Y., Yamamoto K.; "Isolation and sequencing of two cDNA clones encoding rat spleen cathepsin E and analysis of the activation of purified procathepsin
                                          12;
    Length 396;
    38.8%; Score 869; DB 1; Length 39
45.1%; Pred. No. 1.4e-62;
tive 70; Mismatches 136; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPAGPLWILGDVFIROFYSVFDRG----NNRVGLAPA 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPAGPFWILGDVFLGTYVAVFDRGDMKSSARVGLARA 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P16278; 063701; 01-APR-1990 (Rel. 14, Created) 15-J701-1998 (Rel. 36, Last sequence update) 2-J701-1998 (Rel. 36, Last sequence update) 2-J701-203 (Rel. 41, Last annotation update) 2-gthepsin E precursor (EC 3.4.23.34).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               398 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SÜBUNIT: Homodimer; digulfide-linked.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=P16228-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Spleen;
MEDLINE=96004785; PubMed=7574663;
Query Match
Best Local Similarity 45.1%
Matches 179; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FROM N.A.
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364 PPAGPLWILGDVFIRKFYSVFDRG----NNQVGLAPA 396
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DISULFID
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Best Local
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MOD RES
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                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         245 PPLTFVPVTVPAYWQIHMERVKVGPGLTLCAKGCAAILDTGTSLITGPTBEIRALHAAIG 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            245 GSLNWIPVTKQGYWQIALDGIQVGDTVMFCSEGCQAIVDTGTSLITGPPKKIKQLQEAIG 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 PIFVPLSNYRDVQYFGEIGLGTPPQNFTVAFDTGSSNLWVPSRRCHFFSVPCWLHHRFDP 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GINEPLINYLDMEYFGTVSIGSPSONFTVIFDTGSSNLWVPSVYC--TSPACKAHPVFHP 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 KASSSFQANGTKFAIQYGTGRVDGILSEDKLTIGGIKGASVIFGEALWEPSLVFAFAHFD 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GILGLGFPILSVEGVRPPMDVLVEQGLLDKPVFSFYLNRDPEEPDGGELVLGGSDPAHYI 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 305 GIPLLAGEYIILCSEIPKLPAVSFLLGGVWFNLTAHDYVIQTTRNGVRLCLSGFQALDVP 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 LLLLLPLLNVEPSGATLIRIPLHRVQPGRRTL----NLLRGWR-EPAELPKLGAPSPGDK
                                                                                                                                                                                                                                                                                                                                                                                                PYRROLIDONE CARBOXYLIC ACID
(BY SIMILARITY)
BY SIMILARITY
BY SIMILARITY
BY SIMILARITY
INTERCHAIN (PROBABLE).
BY SIMILARITY
BY SIMILARITY
BY SIMILARITY
N-LINKED (GLCNAC. . .) (PROBABLE).
Missing (in isoform Short).
//FIIde=VSp 005224.
P -> S.
E -> N (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
                                                                                                                                                                                                                                                                                                PRINTS; PR00792; PEPSIN.
PROSITE; PS00141; ASP PROTEASE; 2.
Hydrolase; Aspartyl protease; Glycoprotein; Zymogen; Signal;
Alternative spilcing; Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38.7%; Score 867; DB 1; Length 39 45.3%; Pred. No. 2e-62; Live 68; Mismatches 137; Indels
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25F123E67C46EB5F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                      ACTIVATION PEPTIDE.
CATHEPSIN E.
IsoId=P16228-2; Sequence=VSP_005224;
SIMILARITY: Belongs to peptidase family Al.
                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                            MEROPS; A01.010; -.
InterPro; IPR001969; Aspprotease_AS.
InterPro; IPR009007; Pept_A_acid.
InterPro; IPR001461; Peptidase_A1.
Pfam; PF00026; asp; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43021 MW;
                                                                                                                                                       EMBL, D45187; BAA08128.1; -. EMBL, D38104; BAA07285.1; -. PIR, A34657. A34657. A34657. S66465; S66465. HSSP; P00794; 4CMS.
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398
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278
92
344
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274
92
312
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ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                            SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Rabbit procathepsin E and cathepsin E. Nucleotide sequence of cDNA, hydrotytic specificity for biologically active peptides and gene expression during development.";

Eur. J. Biochem. 216:717-728(1993).
-!- FUNCTION: Due of its intracellular location and distribution in lymphoid associated tissue, if may have a role in immune function.
-!- CATALITIC ACTIVITY: Similar to cathepsin D, but slightly broader.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLILLLPLINVEPSGATLIRIPLHRVQPGRRTLNLIRG-----WR-EPAELPKLGAPSPG
                                                                                                                                                                              Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACTIVATION PEPTIDE (BY SIMILARITY)
CATHERSIN B.
PYRROLIDONE CARBOXYLIC ACID
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37.9%; Score 848.5; DB 1; Length 396; 44.9%; Pred. No. 6.2e-61; Live 68; Mismatches 137; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00792; PEPSIN.
PROSITE; PS00141; ASP_PROTEASE; 1.
Hydrolase; Aspartyl protease; Glycoprotein; Zymogen; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     specificity.
-!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: Belongs to peptidase family A1.
                                                  01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
83-FEB-2003 (Rel. 41, Last annotation update)
Cathepsin E precursor (EC 3.4.23.34).
  396 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001969; Aspprotease_AS.
InterPro; IPR009007; Pept A.acid.
InterPro; IPR001461; Peptidase_A1.
Pfam; PF00026; asp; 1.
  PRT;
                                                                                                                                                                                                                                                                                                                                                                            MEDL/INE=94009032; PubMed=8404890;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBI, L08418; AAC37308.1; -. PIR, S36865; S36865.
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STANDARD;
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SEQUENCE FROM N.A.
STRAIN=Japanese white;
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MERCPS; A01.010; -.
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396 AA;
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63 DKPIFVPLSNYRDVQYFGEIGLGTPPQNFTVAFDTGSSNLWVPSRRCHFFSVPCWLHHRF 122
               63 EQSANEPLINYLDMEXFGTISIGSPPQNFTVIFDTVSSNLWVPSVYC--TSPACQMHPQF 120
                                              123 DPKASSSFQANGTKFALQYGTGRVDGILSEDKLTIGGIKGASVIFGFALWEPSLVFAFAH 182
                                                              183 FDGILGLGFPILSVEGVRPPMDVIVEQGLLDKPVFSFYLNRDPEFPDGGELVLGGSDPAH 242
                                                                                                                                              243 YIPPLTFVPVTVPAYWQIHMERVKVGPGLTLCAKGCAAILDTGTSLITGPTBEIRALHAA 302
                                                                                                                                                             241 FSGSLNWVPVTKQGYWQIALDEIQVGGSPMFCPEGCQAIVDTGTSLITGPSDKIIQLQAA 300
                                                                                                                                                                                                                                         363 VPPPAGPFWILGDVFLGTYVAVFDRGDMXSSARVGLARA 401
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Search completed: June 2, 2004, 20:19:35 Job time: 18.3371 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

June 2, 2004, 20:14:10; Search time 28.59 Seconds (Without alignments) 1413.099 Million cell updates/sec Run on:

US-09-700-770-8 2238 1 MSPPPLLQPLILLLPLLNVE......ARTRGADLGWGETAQAQFPG 420 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched:

Total number of hits satisfying chosen parameters:

283366

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	cathebsin D (EC 3.	Ω	Ω		prot	cathebsin D (EC 3.	cal	ίΞ CH	ш	cathebsin E (EC 3.	protein	renin (EC 3.4.23.1	Bin E (EC	EG CE CE	prot	renin (EC 3.4.23.1	Bin	۳. س	(EC 3	(EC 3	cyprosin (EC 3.4.2	-					pepsin A (EC 3.4.2		(EC 3.4.
SUMMARIES	ΩI	151185	KHHUD	KHRTD	KHMSD	A45117	KHPGD	T24204	A34401	S66465	836865	S19697	REMSS	A43356	866516	JC5077	REMSK	S66466	147099	RERTK	REHUK	T12049	T11686	T07915	D85056	JS0732	T09739	S19682	F86253	PEMQAR
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	Length	66	412	407	41	38	34	44	39	39	99	20	40	39	20	44	40	36	400	40	40	47	51	206	20	49	51	38	20	38
de	Query Match	46.0	45.4		44.3	43.1	'n.	ö	38.8	38.7	7.	7.	36.1		ď.	'n.	'n.	5.	35.0	4.	•	4.	4.	٠	4.	4.	34.4	4.	34.2	4.
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JC7272	S71591	S47096	PEHU	S19684	B30142	T33383	PEMOAJ	A30142	S49349	C38302	PEPG	D38302	JC7575	B38302	A41443
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C)	2.	4.0	33.9	33.8	33.8	33.8	33.8	33.7	33.7	32.9	32.9	32.8	32.0	32.0	31.6
34.	3,	C)													
765.5 34.	765 34			757.5	757.5	756	755.5	754.5	754	737	735.5	733	717	717	707.5

ALIGNMENTS

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RESULT 1 151185 cathepsin D (EC 3.4.2 C;Species: Gallus gal C;Date: 04-Sep-1997 C;Access.on: 151185 N;Retzek, H; Steyrer DNA Cell Biol. 11, 66 A;Title: Molecular cl A,Reference number: 1 A,Accession: 151185 A;Status: preliminary A,Rolecula type: mRNA A,Residues: 1-398 «RE A;Cross.references: G;Superfamily: pepsin C;Keywords: aspartic Query Match Best Local Similari	3.5) precursor - chicken lus (chicken) sequence_revision 04-Sep-1997 #text_change 22-Jun-1999 'E.; Sanders, E.J.; Nimpf, J.; Schneider, W.J. 1-672, 1992 oning and functional characterization of chicken catheps 51185; MUID:93039672; PMID:1418623 ; translated from GB/EMBL/DDBJ T> B:849650; NID:g259834; PIDN:AAB24157.1; PID:g259835 proteinase; hydrolase 46.0%; Score 1030; DB 2; Length 398; ty 50.0%; Pred, No. 3.6e-78;
Macciles 21	of conservative 5/; Mismatches 115; indeis 36; Gaps 7;
Oy 1	1 MSPPPLLQPLLLLPLLNVEPSGATLIRIPLHRVQPGRRTLNLLRGWREPAELPKLGA 58
Oy 59	9
00 105	PSRRCHFFSVPCWI.HHRFDPKASSSPOANGTKFAIOVGTGRAVDGII.SEDKI.TIGGIKGAS
	POWERT DISCLIBILIZATION OF THE PROPERTY OF THE PROPERTY OF THE PARTY OF THE PROPERTY OF THE PR
Qy 165 Db 165	S VIFGEALWEPELVFAFAHFDGILGLGFPILSVEGVRPPMDVLVEQGLLDKPVFSFYLNRD 224
Qy 225 Db 225	S PEEPDGGELVLGGSDPAHYIPPLTFVBVTVPAYWQIHWERVKVGPGLTLCAKGCAAILDT 284
Qy 285 Db 285	5 GTSLITGPTEBIRALHAAIGGIPLLAGEYIILGSEIPKLPAVSFLLGGWWFNLTAHDYVI 344
Qy 345 Db 345	5 QTTRNGVRLCLSGFQALDVPPPAGPFWILGDVFLGTYVAVFDRGDMKSSARVGLAR 400 :: :

RESULT

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Accession: Joint, X. Muller, Mang, X.; Wong, R.N.S.; Hartsuck, J.A.; Tang, J. R.Y. S.; Takahashi, T.; Wang, X.; Wong, R.N.S.; Hartsuck, J.A.; Tang, J. S.; Takahashi, T.; Wang, X.; Wong, R.N.S.; Hartsuck, J.A.; Tang, J. S.; Diol. Chem. 263, 16504-16511, 1988
A,Title: Structures at the proteolytic processing region of cathepsin D. A,Reference number: A92681; WUID:89034127; PMID:3182800
A,Accession: C31918
A,Wolecule type: protein
A,Residuce: 134-162, T.', 164-170 «YON»
R;Pujita, H.; Tanaka, Y.; Noguchi, Y.; Kono, A.; Himeno, M.; Kato, K. Biochem. Biophys. Res. Commun. 179, 190-196, 1991
A,Title: Isolation and sequencing of a cDNA clone encoding rat liver lysosomal cathe A,Reference number: JQ1177; WUID:91354249; PMID:1883350
C;Keywords: aspartic proteinase, glycoprotein; hydrolase, lysosome, protein degradat F;1-20/Domain: signal sequence #status predicted <SIG>F;21-64/Domain: propeptide #status predicted <PRO>F;52-64/Domain: propeptide #status predicted <PRO>F;52-62,169-410/Product: cathepsin D #status experimental <MAT>F;55-162,169-410/Product: cathepsin D #status experimental <MAT>F;52-160,110-117,286-290,329-366/Disulfide bonds: #status experimental F;77,295/Active site: Asp #status experimental F;77,295/Active site: Asp #status experimental F;134,263/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                   5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 ACWIHHKYNSDKSSTYVKNGTSFDIHYGSGSLSGYLSQDTVSVPCQSASSASALGGVKVE 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          296 TGTSLMVGPVDEVRELQKAIGAVPLIQGEYMIPCEKVSTLPAITLKLGGKGYKLSPEDYT 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cathepsin D (EC 3.4.23.5) precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Dacession: S13111; C31918; JQ1177; PQ0222
R;Birch, N.P.; Loh, Y.P.
Nucleic Acids Ree: 18, 6445-6446, 1990
A;Title: Cloning, sequence and expression of rat cathepsin D.
A;Ritle: Cloning, sequence and expression of publications of the cathepsin D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SQAVPAVTEGPIPEVLKNYMDAQYYGEIGIGTPPQCFTVVFDTGSSNLWVPSIHCKLLDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MSPPPLLQPLLLLLPLLNVEPSGATLIRIPLHRVQPGRRTLNLLRGWRE-----PAELP
                                                                                                                                                                                                                                                                                                                                                                                                                                                      55 KLGAPSPGDKPIFVPLSNYRDVQYFGEIGLGTPPQNFTVAFDTGSSNLWVPSRRCHFFSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SVIFGEALWEPSLVFAFAHFDGILGLGFPILSVEGVRPPMDVLVEQGLLDKPVFSFYLNR
                                                                                                                                                                                                                                                                                                                                                      26;
                                                                                                                                                                                                                                                                                        Length 412;
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A; Residues: 1-14,'A',16-204,'N',206-261,'N',263-407 <FUJ>
A; Accession: PQ0222
                                                                                                                                                                                                                                                                                                               46.9%; Pred. No. ....
tive 71; Mismatches 125;
                                                                                                                                                                                                                                                                                    45.4%; Score 1015; DB 1; 46.9%; Pred. No. 6.7e-77;
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A;Residues: 65-74;118-127;165-174 <FU2>
                                                                                                                                                                                                                                                                                                                                                   Matches 196; Conservative
                                                                                                                                                                                                                                                                                                                     Best Local Similarity
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A;Molecule type: mRNA
A;Residues: 1-407 <BIR>
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C; Comment: Cathepsin D is a ubiquitous lysosomal proteinase.
C; Comment: In addition to the propeptide, residues 163-168 and 411-412 are proteolytical
C; Comment: The carbohydrate bound to 134-Asn contains a mannose-6-phosphate that is bount
C; Genetics: As Gene: GDB:120512; OMIM:116840
A; Gene: GDB:120512; OMIM:116840
A; Map position: lipl5.5-11pl5.5
A; Description: limited specificity endopeptidase
A; Pathway: intracellular protein degradation
C; Superfamily: pepsin
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Arities Molecular cloning of mouse cathepsin D.
Arrities Molecular cloning of mouse cathepsin D.
Arrities Molecular cloning of mouse cathepsin D.
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R;Cho, W.L.; Raikhel, A.S.
J. Biol. Chem. 267, 21823-21829, 1992
A;Title: Cloning of cDNA for mosquito lysosomal aspartic protease. Sequence analysis
A;Reference number: A45117; MUID:93016141; PMID:1400492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 SDKSSTYVKNGTSFDIHYGSGSLSGYLSODTVSVPCKSDOSKARGIKVEKOIFGEATKOP 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       175 SLVFAFAHFDGILGLGFPILSVEGVRPPMDVLVEQGLLDKPVFSFYLNRDPREPDGGELV 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     245 LGGTDSKYYHGELSYLNVTRKAYWQVHWDQLEVGNELTLCKGGCEAIVDTGTSLLVGFVE 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 KPIFVPLSNYRDVQYFGEIGLGTPPQNFTVAFDTGSSNLWVPSRRCHFFSVPCWLHHRFD 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 235 LGGSDPAHYIPPLIFVPVTVPAYWOIHMERVKVGPGLILCAKGCAAILDIGISLIIGPTE 294
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C;Species: Aedes aegypti (yellow fever mosquito)
C;Date: 1.7-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 LLLLLPLLNVEPSGATLIRIPLHRVQPGRRTLNLLRGWRE------PAELPKLGAPSPGD
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                         A;Cross-references: EMBL:X53337; NID:g50300; PIDN:CAA37423.1; PID:g50301 K;Grusby, M.G., Mitchell, S.C.; Glimcher, L.H. Nucleic Acids Res. 18, 4008, 1990 A;Title: Molecular cloning of mouse cathepsin D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 44.3%; Score 992.5; DB 1; Length 410; Best Local Similarity 47.7%; Pred. No. 5e-75; Matches 194; Conservative 67; Mismatches 125; Indels 21
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A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-387 <CHC
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A; Experimental source: liver
C; Comment: Cathepsin D in rat liver lysosome occurs as a mixture of both a single chain
C; Function:
A; Description: limited specificity endopeptidase
A; Pathway: intracellular protein degradation
C; Superfamily: pepsin
C; Superfamily: pepsin
C; Superfamily: pepsin
C; Keywords: aspartic proteinase; glycoprotein; hydrolase; lysosome; protein degradation
C; Keywords: aspartic proteinase; glycoprotein; hydrolase; lysosome; protein degradation
C; Keywords: aspartic proteinase; glycoprotein; hydrolase; lysosome; protein degradation
F; 1-20/Domain: signal sequence #status predicted <BRO>
F; 21-64/Domain: propeptide #status predicted <ARO>
F; 55-164/Product: cathepsin D, 43K single-chain form #status predicted <ARA>
F; 65-117/Product: cathepsin D 9K light chain #status predicted <ARA>
F; 65-107/Product: cathepsin D 34K leavy chain #status predicted <ARA>
F; 165-407/Product: (or 166-407) cathepsin D 30K heavy chain #status predicted <ARA>
F; 165-407/Product: cathepsin D 34K heavy chain #status predicted
F; 97, 290/Active site: Asp #status predicted
F; 97, 250/Active site: Asp #status predicted
F; 134, 258/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Sate: 31-Dec-1991 #sequence restsion 31-Dec-1991 #text_change 18-Jun-1999
C.Accession: 148279; S14704; Saffig, P.; Von Figura, K.; Peters, C.
DNA Cell Biol. 13, 419-427, 1994
A.Fitle: Mouse cathepsin D gene: molecular organization, characterization of the p. A.Reference number: 148278 MID:94280622; PMID:801168
A.Reference number: 148278 MID:94280622; PMID:8011168
A.Residues: 1-410 - RES-A.References: EMBL.X68378; NID:950302; PIDN:CAA48453.1; PID:9817945
A.Cross-references: EMBL.X68378; NID:950302; PIDN:CAA48453.1; PID:9817945
A.Residues: 1-410 - RES-A.Reference of a cDNA encoding mouse cathepsin D.
A.Reference number: S14704; MUID:91088345; PMID:2263503
A.Accession: S14704
A.Molecule type: mRNA
A.Residues: 1-410 - DIE-A.Residues: 1-410 - DIE-A.Resi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               244
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Matches 196; Conservative
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A;Cross-references: GB:M95187; NID:g293229; PIDN:AAA29350.1; PID:g293230 A;Experimental source: fat body A;Note: Hequence extracted from NCBI backbone (NCBIN:116753, NCBIP:116754)

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Local Similarity
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Cathepsin D (EC 3.4.23.5) - pig
Cipecies Sus scrofa domestica didomestica pig)
Cipecies Sus scrofa domestica all-Dec-1991 #text_change 18-Mar-1997
Cipaces 108-Apr-1804 #sequence revision 31-Dec-1991 #text_change 18-Mar-1997
R; Tachabshi, T. i Tang, J.
B; Tachabshi, T. i Tang, J.
J. Biol. Chem. 258, 6435-6443, 1983
A; Title Amino acid sequence of porcine spleen cathepsin D light chain.
A; Reservence number: A3-2455; MUD:83213348; PMID:6406481
A; Roseidaes 1.95, S. y 7, Taxx
A; Roseidaes 1.95, S. y 7, Tang, Y.
A; Roseidaes 1.95, S. y 7, Taxx
A; Roseidaes 1.95, S. y 9, Taxx
A; Roseidaes 1.95, S. y 109-84
A; Roseidaes 1.95, S. y 109-85
A; Roseidaes 1.95
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                                                                                                                                                                                    6 LLOPLILLIPLINVEPSGATLIRIPLHRVQPGRRTLNLLRGWREPAELPKLGAPSPGDKP
                                                                                                                                             Gaps
                                                                                                                                           11;
                                                                                                Length 387;
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                                                                                                                                         62; Mismatches 131;
C;Superfamily: pepsin
C;Keywords: aspartic proteinase; hydrolase; lysosome
F;86,272/Active site: Asp #status predicted
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                                                                                                                                         Conservative
                                                                                           Query Match
Best Local Similarity
Matches 192; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              296 IRALHAAIGGIPLLAGEYIILCSEIPKLPAVSFLLGGVWFNLTAHDYVIQTTRNGVRLCL 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residudes: 1-444 «MIL»
A;Cross-references: EMBL:250755; PIDN:CAA90633.1; GSPDB:GN00028; CESP:R12H7.2
A;Experimental source: clone R12H7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein R12H7.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Decies: Caenorhabditis elegans
C;Decies: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T24204
R;Coles, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIFVPLSNYRDVQYFGEIGLGTPPQNFTVAFDTGSSNLWVPSRRCHFFSVPCWLHHRFDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGSDPAHYIPPLTFVPVTVPAYWQIHMERVKVGPGLTLCAKGCAAILDTGTSLITGPTEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 FQANGTKFAIQYGTGRVDGILSEDKLTIGGIKGASVIFGEALWEPSLVFAFAHFDGILGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GFPILSVEGVRPPMDVLVEQGLLDKPVFSFYLNRDPEEPDGGELVLGGSDPAHYIPPLTF
                                                                                                                                                                                                                                                                                                                                                          PIPEVLKNYMDAQYYGEIGIGTPPQCFTVVFDTGSSNLWVPSIHCKLLDIACWIHHKYNS
                                                                                                                                                                                                                                                                                                                                                                                                                KASSSFQANGTKFALQYGTGRVDGILSEDKLT----IGGIKGASVIFGEALWEPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LVFAFAHFDGILGLGFPILSVEGVRPPMDVLVEQGLLDKPVFSFYLNRDPEEPDGGELVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGIDSKYYKGSLDYHNVTRKAYWQIHMNQVAVGSSLTLCKGGCEAIVDTGTSLIVGQPEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70 LSNYRDVQYFGEIGLGTPPQNFTVAFDTGSSNLWVPSRRCHFFSVPCWLHHRFDPKASSS
                                                                                                                                                                                                                                                   Gaps
                                                                                                               experimental
F;1-97/Product: cathepsin D light chain #status experimental <CDL>
F;103-34;Product: cathepsin D heavy chain #status experimental <CDH>
F;33,229/Active site: Asp #status experimental
F;46-53,220-224,263-300/Disulfide bonds: #status predicted
F;46-170,197/Binding site: carbohydrate (Asn) (covalent) #status experiment
F;287/Binding site: carbohydrate (Asn) (covalent) #status absent
                                                                                                                                                                                                                                                13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5,
                                                                                                                                                                                          Length 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGFQALDVPPPAGPFWILGDVFLGTYVAVFDRGDMKSSARVGLARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                       Query Match
42.6%; Score 954.5; DB 1;
Best Local Similarity 52.9%; Pred. No. 5.9e-72;
Matches 183; Conservative 48; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1e-67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40.5%; Score 905.5; I
49.7%; Pred. No. 1e-67
ive 58; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted to the EMBL Data Library, August 1995
A;Reference number: Z19854
A;Accession: T24204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Map position: X
A;Introns: 29/2; 91/3; 133/1; 214/1; 395/2
C;Superfamily: pepsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 49.7
Matches 166; Conservative
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(in mature form) (probably pyrrolidone ca
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C;Species: Rattus norvegicus (Norway rat)
C;Species Cat.1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C;Accession: S66465; S74309
R;Okamotc, K.; Yu, H.; Misumi, Y.; Ikehara, Y.; Yamamoto, K.
Arch. Bicchem. Biocham. Bio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 KASSSFQANGTKFAIQYGTGRVDGILSEDKLTIGGIKGASVIFGEALWEPSLVFAFAHFD 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 PIFVPLSNYRDVQYFGEIGLGTPPQNFTVAFDTGSSNLWVPSRRCHFFSVPCWLHHRFDP 124
                                                                                                                                                                                                                                                                                                                                                                                                                                         124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 SQSSTYSQPGQSFSIQYGTGSLSGIIGADQVSVBGLTVVGQQFGESVTEPGQTFVDAEFD 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243 GSLNWVPVTKQAYWQIALDNIQVGGTVMFCSEGCQAIVDTGTSLITGFSDKIKQLQNAIG 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GIPLLAGEYIILCSEIPKLPAVSFLLGGVWFNLTAHDYVIQTTRNGVRLCLSGFQALDVP 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 LILLILLILLDLAQAQGVLHRVPLRRHQSLRKKLRAQGQLSDFWRSHNLDMIEFSESCNVDK 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:D45187; NID:g1113085; PIDN:BAA08128.1; PID:g1113086
A;Accession: S74309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 SAKEPLINYLDMEYFGTISIGSPPQNFTVIFDTGSSNLWVPSVYC--TSPACKTHSRFQP
                                                                                                                                                                                                                                                                               10 ILLILIPLINVEPSGATLIRIPLHRVQPGRRTL----NLLRGWR-EPAELPKLGAPSPGDK
                                                                                                                                                                                                                                                                                                                                 65 PIFVPLSNYRDVQYFGEIGLGTPPQNFTVAFDTGSSNLWVPSRRCHFFSVPCWLHHRFDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 KASSSFQANGTKFALQYGTGRVDGILSEDKLTIGGIKGASVIFGEALWEPSLVFAFAHFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GILGLGFPILSVEGVRPPMDVLVEQGLLDKPVFSFYLNRDPEEPDGGELVLGGSDPAHYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            245 PPLTFVPVTVPAYWQIHMBRVKVGPGLTLCAKGCAAILDTGTSLITGPTBBIRALHAAIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 LILLLPLINVEPSGATLIRIPLHRVQPGRRTL----NLLRGWR-BPAELPKLGAPSPGDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
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                                                                                                                    Query Match 38.8%; Score 869; DB 2; Length 39 Best Local Similarity 45.1%; Pred. No. 9.6e-65; Matches 179; Conservative 70; Mismatches 136; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68; Mismatches 137; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Keywords: aspartic proteinase; hydrolase
F;1-19,70main: signal sequence #status predicted <SIG>
F;20-58/Domain: propeptide #status experimental <PRO>
F;20-398/Product: cathepsin E #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |||||| ||||||||| : :||||| |
PPAGPLWILGDVFIRQFYSVFDRG----NNRVGLAPA 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPAGPFWILGDVFLGTYVAVFDRGDMKSSARVGLARA 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 38.7%; Score 867; DB 2; Similarity 45.3%; Pred. No. 1.4e-64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----
F_118/Modified site: blocked amino end (Gln) F_196,281/Active site: Asp #status predicted
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A, Residues: 20-47,59-91 <OKM>
C, Superfamily: pepsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: mRNA
A;Residues: 1-398 <OKA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: S66465
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Best Local 3
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A/Molecule type: DNA
A/Residues: 1-396 cAZUS
A/CROSS-references: GB:M84424; GB:M82847; NID:g181203; PIDN:AAA52300.1; PID:g181205
A/Residues: 1-396 cAZUS
A/CROSS-references: GB:M84424; GB:M82847; NID:g181203; PIDN:AAA52300.1; PID:g181205
A/Rote: sequence extracted from NCBI backbone (NCBIN:75964, NCBIN:75966, NCBIN:75971, NG
B.A. Chem. 264, 16748-16753, 1989
A/Title: Human gastric cathepsin E. Predicted sequence localization to chromosome 1, and
A/Reference number: A34401
A/Accession: A34401
A/Accession: A34401
A/Rolecule type: mRNA
A/Residues: 1-396 cAZ2
A/Takeds-Ezaki, M.; Yamanoto, K.
A/Takeds-Ezaki, M.; Yamanoto, K.
A/Takeds-Ezaki, M.; Yamanoto, K.
A/Title: Isolation and biochemical characterization of procathepsin E from human erythro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: 334467
A;Status: preliminary
A;Nolecule type: protein
A;Residues: 57-60,62-81 cHIL>
B;Athauda, S.B.P.; Matsuzaki, O.; Kageyama, T.; Takahashi, K.
B;Athauda, S.B.P.; Matsuzaki, O.; Kageyama, T.; Takahashi, K.
A;Athauda, S.B.P.; Matsuzaki, O.; Kageyama, T.; Takahashi, K.
A;Athauda, S.B.P.; Matsuzaki, O.; Kageyama, T.; Takahashi, K.
A;Title: Structural evidence for two isozymic forms and the carbohydrate attachment site
A;Reference number: A34643; MUID:90241267; PMID:2334440
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A34401

BA34401

Catchepsin E (EC 3.4.23.34) precursor - human

C;Species: Homo sapiens (man)

C;Date: 22-Unn-1990 #sequence revision 22-Unn-1990 #text_change 22-Unn-1999

C;Date: 22-Unn-1990 #sequence revision 22-Unn-1990 #text_change 22-Unn-1999

C;Accession: A42038, A34401; S35663; S34467; A34643; B34643

R;Azuma, T.; Liu, W.; Vander Laan, D.J.; Bowcock, A.M.; Taggart, R.T.

J; Biol. Chem. 267, 1609-1614, 1992

A;Title: Human gastric cathepsin B gene. Multiple transcripts result from alternative pareference number: A42038; MUID:92112877; PMID:1370478
                                                          266 VPVTRKGYWQFKMDKV-VGSGVLGCSNGCQAIADTGTSLIAGFKAQIEAIQNFIGAEPLI 324
                                                                                                                                                                  310 AGEYIILCSEIPKLPAVSFLLGGVWFNLTAHDYVIQTTRNGVRLCLSGFQALDVPPPAGP 369
                                                                                                                                                                                                            325 KGEYMISCDKVPTLPPVSFVIGGQEFSLKGEDYVLKVSQGGKTICLSGFMGIDLPERVGE 384
            VPVTVPAYWQIHMERVKVGPGLTLCAKGCAAILDTGTSLITGPTEEIRALHAAIGGIPLL 309
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A, Residues: 54-58, XXX', 62-64, 'M', 66-89, 'X', 91-95 < ATH>
A, Accession: B34643
A, Accession: B34643
A, Status: preliminary
A, Molecule type: protein
C, Genetics:
A, Gene: GDB: CTSE
A, Cross-references: GDB: 119821; OMIM: 116890
A, Cross-references: GDB: 119821; OMIM: 116890
C, Superfamily: pepsin
C, Superfamily: pepsin
C, Superfamily: pepsin
C, Superfamily: pepsin
C, Reywords: aspartic proteinase; blocked amino end; hydro
C, Reywords: aspartic proteinase; blocked amino end; hydro
F, 1-17/Domain: activation peptide #status predicted < SIG>F; 18-53/Domain: activation peptide #status predicted < PRF
F; 54-396/Product: cathepsin E #status predicted < PRE
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A; Status: preliminary
A; Molecule type: Protein
A; Residues: 20-38; 54-76 < TAX>
R; Hill, J.; Montgomery, D.S.; Kay, J.
R; Hill, J.; Montgomery, D.S.; Kay, J.
A; Title: Human cathepsin E produced in B. coli.
A; Reference number: S34467; MUID:99314762; PMID:8325357
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A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              HREDPKASSSFRANGTKFALOYGTGRVDGILSEDKLTIGGIKGASVIFGEALWEPSLVFA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Hordeum vulgare (barley)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 22-Jun-1999
C;Accession: S19697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PKHYVGEHTYVPVTQKGYWQFDWGDVLVGGKSTGFCAGGCAAIADSGTSLLAGPTALITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             305 INEKİGAAGVVSQECKTIVSQYGQQILDLLLAETQPKKICSQVGLCTFDGTRGVSAGIRS
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                                                                                                                                                                                                                                                                                                                                                              10 ILLAAVILLQTVI.PAASEAEGLVRIALKK-RPIDRNSRVATGLSGGEEQPLLSGANPLRSE
                                                                                                                                                                                                                                                                                                                                        6 LLQPLALLLPLIAVEPSGATLIRIPLHRVQPGRRTLNLLRGWREPAELPKLGAPSP----
                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 36.7%; Pred. No. 2.4e-61;
Matches 186; Conservative 54; Mismatches 147; Indels 1:
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Hordeum vulgare (barley)
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S18665
Cathepsin E (EC 3.4.23.34) precursor - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 10-Dec-1993 #sequence_revision 27-Feb-1997 #text_change 22-Jun-1999
C;Date: 10-Dec-1993 #sequence_revision 27-Feb-1997 #text_change 22-Jun-1999
C;Accession: 836865
R;Kageyama, T.
Eur. J. Bulcohen. 216, 717-728, 1993
A;Reference number: 216, 717-728, MUID:9409032; PMID:8404890
A;Reference number: 836865, MUID:9409032; PMID:8404890
A;Restues: preliminary
A;Molecule type: mRNA
A;Residues: 1-396 < KAG>
A;Cession: 28665
A;Cession: 28665
A;Cession: 1-396 < KAG>
C;Superfamily: pepsin
C;Keywords: aspartic proteinase; hydrolase
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                                                   245 GSLNWIPVTKQGYWQIALDGIQVGDTVWRCSEGCQAIVDTGTSLITGPPKKIKQLQEAIG 304
                                                                                                                                                   GIPLLAGEYIILCSEIPKLPAVSFLLGGVWFNLTAHDYVIQTTRNGVRLCLSGFQALDVP 364
                                                                                                                                                                     62
                                 GILGLGFPILSVEGVRPPMDVLVEQGLLDKPVFSFYLNRDPEEPDGGELVLGGSDPAHYI 244
                                                                                         245 PPLTFVPVTVPAYWQIHMERVKVGPGLTLCAKGCAAILDTGTSLITGPTEEIRALHAAIG 304
   SQSSTYMEVGNHFSIQYGTGSLTGIIGADQVSVEGLTVEGQQFGESVKEPGQTFVNAEFD 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 PLILILI-LIDLGQAQGTLDRVPLRR-OPSLRKKCRAQGQLSBFWKAHKVDMVQYTETCTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 RPSQSNTYSEVGTPFSIAYGTGSLTGIIGADQVSVQGLTVVGQQFGBSVKEPGQTFVNAB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 PLILLILPLINVEPSGATLIRIPLHRVQPGRRTLNLLRG----WR-EPAELPKLGAPSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
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44.9%; Pred. No. 5e-63;
iive 68; Mismatches 137;
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Conservative 6
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179; Conserv
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Matches 17
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304 305 364 -----IPLLAGEYI 314

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renin (EC 3.4.23.15) precursor, submandibular - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 15-0ct-1982 #sequence_revision 17-Dec-1982 #text_change 18-Jun-1999
C;Accession: A93923, A93285; B93285; B22088; A00988
R;Misonc, K.S.; Chang, J.J.; Inagami, T.
Proc. Natl. Acad. Sci. U.S.A. 79, 4880-4862, 1982
A;Title: Amino acid sequence of mouse submaxillary gland renin.
A;Reference number: A93923; MUID:83014991; PMID:6812055
A;Accession: A93823
A;Molecule type: protein
A;Residues: 64-351;354-401 cMIS>
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aspartic proteinase (EC 3.4.23.-) precursor - barley

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cathepsin E (EC 3.4.23.34) precursor - guinea pig
NyAlternate names: erythrocyte membrane aspartic proteinase; slow-moving proteinase
C,Species: Cavia porcellus (guinea pig)
C,Becciss: Cavia porcellus (guinea pig)
C,Accession: A43356
R,Rageyama, T.; Ichinose, M.; Teukada, S.; Miki, K.; Kurokawa, K.; Koiwai, O.; Tanji
J, Biol. Chem. 267, 16450-16459, 1932
A;Title: Gastric procathepsin E and progastricsin from guinea pig. Purification, mol.
A;Reference number: A43356; MUID:92355614; PMID:1644829
A;Accession: A43356
A;Molecule type: mRNA
A;Residuse: 1.391 < KAG>
A;Rosiduse: 1.391 < KAG>
A;Cross-zeferences: GB:N88653; NID:g191294; PIDN:AAA37052.1; PID:g191295
A;Note: sequence extracted from NCBI backbone (NCBIN:110763, NCBIP:110769)
C;Superfamily: pepsin
C;Keywords: aspartic proteinase; hydrolase; membrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                184
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-509 <ASZ>
A;Cross-references: EMBL:D32144; NID:g1255684; PIDN:BAA06875.1; PID:g1711289 C;Comment: The pair of saposin repeat homology domains tagged SAP1 and SAP2 c;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oryzaain (EC 3.4.23.-) precursor - rice
N;Alernate names: aspartic proteinase 1
C;Species: Oryza sastiva (frice)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C;Accession: 866516; 866517
R;Asakura, T.; Matanabe, H.; Abe, K.; Arai, S.
Bur. J. Biochem. 232, 77-83, 1995
Bur. J. Biochem. 232, 77-83, 1995
A;Title: Rice aspartic proteinase, oryzasin, expressed during seed ripening
A;Reference number: 866516; MUID:96048031; PMID:7556174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             125 KASSSFQANGTKFALQYGTGRVDGILSEDKLTIGGIKGASVIFGRALWEPSLVFAFAHFD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 LLLLLPLLNVEPSGATLIRIPLHRVQPGRRTL----NLLRGWR-EPAELPKLGAPSPGDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIFVPLSNYRDVQYFGEIGLGTPPQNFTVAFDTGSSNLWVPSRRCHFFSVPCWLHHRFDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             357 PPAGPLWILGDVFIRQFYAVFDRG----NNRVGLAPA 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72; Mismatches 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36.0%; Score 806.5; DB 2; 42.8%; Pred. No. 1.6e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPAGPFWILGDVFLGTYVAVFDRGDMKSSARVGLARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 42.84
Matches 170; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: S66516
A; Molecule type: DNA
A; Residues: 1-509 <ASA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         245
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R;Panthier, J.J.; Foote, S.; Chambraud, B.; Strosberg, A.D.; Corvol, P.; Rougeon, F. Mattree 298, 30-22, 1982.

A;Title: Complete amino acid sequence and maturation of the mouse submaxillary gland ren A;Reference number: A93285, MUID:82220074; PMID:6283773

A;Roccession. A93285

A;Moccession. A93285

A;Moccelle type: mRNM.
A;Residues: 1-38, W.,100-194, 'LGRS',199-194,'V',386-401 PIDNAAA40050.1; PID:9200702

A;Roccession. B93286

A;Roccession. B93286

A;Roccession. B93286

A;Roccession. B93286

A;Residues: 64-64;584-774 PRD.
A;Residues: 64-64;584-774 PRD.
A;Residues: 64-64;584-774 PRD.
A;Residues: 64-64;584-774 PRD.
A;Residues: 64-64;584-77 PRD.
A;Reference number: A93439; WUID:83299090; PMID:6350284
A;Reference number: A93439; WUID:83299090; PMID:6350284
A;Contents: annotation; fatty acid binding renes differ in their 5' putative reg
A;Contents: annotation; fatty acid binding renes differ in their 5' putative reg
A;Contents: annotation; fatty acid binding renes differ in their 5' putative reg
A;Contents: number: A22059; WUID:8429816; PMID:6089205
A;Accession: B2058
A;Molecule type: DMA
A;Reference number: A22059; WUID:8429816; PMID:6089205
C;Comment: Submandibular renin has catalytic and antigenic activities similar to renal recomment: Submandibular renin has catalytic and antigenic activities similar colorents and sequence #status predicted A2075
C;Comment: Submandibular renin has catalytic and antigenic activities similar activation peptide #status predicted A2075
C;Comment: Submandibular senin, submandibular, light chain #status experimental RESI>P;24-63/Domain: addrence #status predicted A2075
F;34-77-281,72-21/Pomain: addrence #status predicted A2075
F;101,286/Accive site: App #status predicted
F;101,286/Accive site: App #status reparamental
F;114-121,277-281,320-357/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FLYLACGIHSLYESSDSSSYMENGDDFTIHYGSGRVKGFLSQDSVTVGGIT-VTQTFGEV 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GELVLGGSDPAHYIPPLTFVPVTVPAYWQIHMERVKVGPGLTLCAKGCAAILDTGTSLIT 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GEVVLGGSDPEHYQGDFHYVSLSKTDSWQITMKGVSVGSSTLLCEEGCEVVVDTGSSFIS 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             294 APTSSLKLIMQALGAKEKRLHEYVVSCSQVPTLPDISFNLGGRAYTLSSTDYVLQYPNRR 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLLQPLLLLLPLLNVEPSGATLIRIPLHRVQPGRRTLNLLRGWREPAELPKLGAP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----SPGDKPIFVPLSNYRDVQYFGEIGLGTPPQNFTVAFDTGSSNLWVPSRRCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LWEPSLVFAFAHFDGILGLGFPILSVEGVRPPMDVLVEQGLLDKPVFSFYLNRDPEEPDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 36.1%; Score 808.5; DB 1; Length Best Local Similarity 41.7%; Pred. No. 1.1e-59; Matches 172; Conservative 62; Mismatches 147; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ŋ
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A;Introns: 119/3; 140/1; 171/3; 209/2; 265/3; 279/1; 300/3; 338/3; 360/2; 412/3; 452/ C;Superfamily: oryzasin; saposin repeat homology

13

RESULT A43356

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7; Gaps

Indels

Mismatches 126;

44;

Conservative

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160;
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                                                                                                                                                                                   а
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          484
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                                                                                                                                                                                                                                                                                                                    185 MVAKFDGILGLGFQEISVGDAVPUWYKNVEQGLVSEPVFSFWFNRHSDEGEGGEIVFGGM 244
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                                                                                                                                                                                                                                                                                               61 --PGDKPIFVPLSNYRDVQYFGRIGLGTPPQNFTVAFDTGSSNLWVPSRRCHFFSVPCWL 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DPAHYIPPLTEVPVTVPAYWQIHMERVKVGPGLT-LCAKGCAAILDTGTSLITGPTEEIR 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EINEKİĞATGVVSQECKTVVSQYGQQILDLLLAETQPSKICSQVGLCTFDGKHGVSAGIK 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SVDCGSLASMPEISFTIGAKKFALKPEFYILKVGEGAAAQCISGFTAMDIPPPRGFLWIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                 179 AFAHFDGILGLGFPILSVEGVRPPMDVLVEQGLLDKPVFSFYINRDPEEPDGGELVLGGS
                                                                                                                                                                                                                        LLOPLILLIPLINVEPSGAT -- LIRIPLHR -- VOPGRRTINLIRGWREPAELPKLGAPS -
                                                                                                                                                                                                                                                HHR FDPKASSSFQANGTKFALQYGTGRVDGILSEDKLTIGGIKGASVIFGEALWEPSLVF
 C;Keywords: aspartic proteinase; hydrolase
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-68/Domain: propeptide #status predicted <PRO>
F;68-509/Product: aspartic proteinase 1 #status predicted <WAT>
F;316-51/Domain: saposin repeat homology #status atypical <SAPI>
F;370-420/Domain: saposin repeat homology #status atypical <SAPI>
F;103,290/Active site: Asp #status predicted
                                                                                                                                                Length 509;
                                                                                                                                            Query Match
Best Local Similarity 36.4%; Pred. No. 3.6e-59;
Matches 185; Conservative 51; Mismatches 146; Indels
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C; Accession: UC5077
R; Harrop, S.A.; Prociv, P.; Brindley, P.J.
B; Harrop, S.A.; Procive and the hookworm A; Reference number: UC5077; MUID:97011129; PMID:8858139
A; Accession: UC5077
A; Residues: 1-442 cHAR>
A; Residues: 1-442 cHAR>
A; Residues: GB:U34888; NID:91507724; PIDN:AAB06575.1; PID:91507725
C; Comment: This enzyme is allergeneic in human and contributes to the segmental inflamma

Length 442;

Score 803.5; DB 2; Pred. No. 3.3e-59;

35.9%;

Query Match Best Local Similarity

Superfamily: pepsin Keywords: aspartic proteinase; hydrolase 106,296/Active site: Asp #status predicted

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189
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                          139
                                                                                                                                                                                                                                              FQANGTKFAIQYGTGRVDGILSEDKLTIGGIKGASVIFGFALWEPSLVFAFAHFDGILGL
                                                                                                              GFPILSVEGVRPPMDVLVEQGLLDKPVFSFYLNRDPEEPDGGELVLGGSDPAHYIPPLTF
                                                                                                                                                                     250 VPVTVPAYWQIHMERVKVGPGLTLCA---KGCAAILDTGTSLITGPTEBIRALHAAIGGI
                                                                                                                                                                                                                            PLILAGEYIILCSEI PKL PAVSFLLGGVWFNLTAHDYVIQTTRNGVRLCLSGFQALDVPPP
70 LSNYRDVQYFGEIGLGTPPQNFTVAFDTGSSNLWVPSRRCHFFSVPCWLHHRFDPKASSS
                                                                                                                                                                                                                                                                                                   380 IGELWILGDVFIGKYYTVFDVG----QARLGFAQAKS 412
                                                                                                                                                                                                                                                                                    AGPFWILGDVFLGTYVAVFDRGDMKSSARVGLARART 403
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Job time : 29.59 secs
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US-09-968-415-4
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Sequence 3, Appl
Sequence 15, Appl
Sequence 44, Appl
Sequence 66, Appl
Sequence 66, Appl
Sequence 670, Appl
Sequence 670, Appl
Sequence 670, Appl
Sequence 670, Appl
Sequence 87, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Appli
Sequence 4, Appli
Sequence 30, Appl
                                                                                                                             (without alignments)
1578.054 Million cell updates/sec
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                                                                                                                                                                                                    2238
1 MSPPPLLQPLLLLPLLNVE.....ARTRGADLGWGETAQAQFPG 420
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                                                                                                          June 2, 2004, 20:19:10 ; Search time 74.8784 Seconds
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1: \cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: \cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: \cgn2_6/ptodata/2/pubpaa/ISO6_NEW_PUB.pep:*
4: \cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
5: \cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
6: \cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
7: \cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: \cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: \cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
11: \cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
11: \cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
12: \cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
13: \cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
14: \cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
15: \cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
16: \cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
16: \cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
16: \cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
17: \cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
18: \cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
18: \cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
18: \cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 US-09-968-415-4

4 US-10-180-719-4

US-09-288-222A-30

US-09-968-899-11

US-09-969-384-15

US-09-969-384-15

US-09-915-582-66

US-09-915-582-66

US-09-915-582-66

US-09-915-302-670

US-09-925-302-670

US-09-925-302-670

US-09-915-882-87

US-09-915-882-87

US-09-915-882-87

US-09-915-882-87
                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                    1155919 segs, 281338677 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                      - protein search, using sw model
                                                                                                                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                               seq length: 0 seq length: 2000000000
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1401011
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Match Length DB
                                                                                                                                                                                   US-09-700-770-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Perfect score:
                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2238
2233
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2233
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Maximum DB
                                                                      OM protein
                                                                                                                                                                                                                            Seguence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database
                                                                                                          Run on:
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Sequence 710, App		12,	e 39,	12,	25	406	Sequence 433, App	969	7	22,	13,	e 9,	13,	179	54,	Sequence 22, Appl	707	631	1,	'n	245		164,		46548	66071		56631,		
3-24	-450-2	3-956	ė	-10-114-464	3-601-091-2		US-10-112-944-433		US-10-220-083-2	US-09-215-450-22	US-09-953-956-13		-110-	-295-027-1	US-10-188-832-54	-109-01-	US-09-833-245-707	US-10-106-698-6317	51-	-10-339-3	2	-10-	US-10-051-874-164	US-10-074-978A-134	10-425-11	US-10-425-114-66071	US-10-425-114-65101	US-10-425-114-56631	US-10-425-114-57054	
11	σ	σ	12	13	16	16	12	15	14	σ	σ	12	13	15	16	16	디	14	14	14	12	12	15	15	12	17	12	12	12	
410	412	412	412	412	412	412	440	444	446	396	396	396	396	396	396	396	368	404	514	514	507	523	376	374	513	513	480	513	Н	
46.3	45.4	45.4	45.4	45.4	45.4	45.4	44.8	40.5	39.6		38.8	38.8	38.8	38.8	38.8	38.8	æ	38.8	7.		9	35.7	•	'n.	•	ď.	35.2	ů,	ď.	
1037	1015	1015	1015	1015	1015	1015	1002		œ	869	S	9	G	G	o	869	868	868	828.5	N	815	798.5	793	790	788	788	787	787	786	
16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

```
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                      Yue, Henry
Guegler, Karl J.
Corley, Neil C.
Tang, Tom Y.
Shab, Purvi
TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
                                                                                                                                                                                                                                                                                                ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Mohan-Peterson, Sheela
REGISTRATION NUMBER: 41,201
REFERENCE/DOCKET NUMBER: PF-0458 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-655-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/968,415
PRIOR TRING DATE: 26-8ep-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/659,151
Sequence 4, Application US/09968415
Publication No. US20020086334A1
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 24 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                      STATE: CA
COUNTRY: USA
```

Sequence 1471, Ap Sequence 87, Appl

```
RESULT 3
US-10-288-222A-30
Squence 30, Application US/1028822A
Squence 30, Application No. US20030119742A1
GENERAL INFORMATION:
APPLICANT: Logan, Thomas Joseph
APPLICANT: Chun, Miyoung
TITLE OF INVENTION: Cardiovascular Disease Using 139, 258, 1261, 1486, 2398, 241
TITLE OF INVENTION: Cardiovascular Disease Using 139, 258, 1261, 1486, 2398, 241
TITLE OF INVENTION: 10183, 10550, 12680, 17921, 33248, 60489 OR 93804
FILE REFERENCE: MPI2001-286PIR(M)
CURRENT APPLICANTION NUMBER: US/10/288,222A
CURRENT PILING DATE: 202-11-05
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 PGDKPIFVPLSNYRDVQYFGEIGLGTPPQNFTVAFDTGSSNLWVPSRRCHFFSVPCWLHH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 AHYIPPLIFVPVIVPAYWQIHMERVKVGPGLILCAKGCAAILDIGISLIIGPTEBIRALH 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAIGGIPLLAGEYIILCSEIPKLPAVSFLLGGVWFNLTAHDYVIQTTRNGVRLCLSGFQA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 AAIGGIPLLAGEYIILCSEIPKLPAVSFLLGGVWFNLTAHDYVIQTTRNGVRLCLSGFQA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361 LDVPPPAGPFWILGDVFLGTYVAVFDRGDMKSSARVGLARARTRGADLGWGETAQAQFPG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 AHFDGILGLGFPILSVEGVRPPMDVLVEQGLLDKPVFSFYLNRDPEEPDGGELVLGGSDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 AHYIPPLIFVPVTVPAYWQIHMERVKVGPGLTLCAKGCAAILDTGTSLITGPTBBIRALH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MSPPPLLQPLLLLLPLLLNVEPSGATLIRIPLHRVQPGRRTLNLLRGWREPAELFKLGAFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 PGDKPIFVPLSNYRDVQYFGEIGLGTPPQNFTVAFDIGSSNLWVPSRRCHFFSVPCWLHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AHFDGILGLGFPILSVEGVRPPMDVLVEQGLLDKPVFSFYLNRDPEEPDGGELVLGGSDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MSPPPLLQPLLLLLPLLNVEPSGATLIRIPLHRVQPGRRTLNLLRGWREPAELPKLGAPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 RFDPKASSSFQANGTKFAIQYGTGRVDGILSEDKLTIGGIKGASVIFGEALWEPSLVFAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 100.0%; Score 2238; DB 14; Best Local Similarity 100.0%; Pred. No. 1.9e-209; Matches 420; Conservative 0; Mismatches 0;
                                                            ATORNEY, AGENT INFORMATION:
ATTORNEY, AGENT INFORMATION:
NAME: Mohan-Peterson, Sheela
REGISTRATION NUMBER: 41,201
REFERENCE, DOCKERT NUMBER: PF-0458 US
TELEPRONICATION INFORMATION:
TELEPRONIC 50-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLONE: 877617
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
APPLICATION NUMBER: US/10
FILING DATE: 25-Jun-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 420 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIBRARY: LUNGAST01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 420; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-183-719-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 AHYIPPLIFVPVIVPAYWQIHMERVKVGPGLILCAKGCAAILDIGTSLIIGPTEEIRALH 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 AAIGGIPLLAGEYIILCSEIPKLPAVSFLLGGVWFNLTAHDYVIQTTRNGVRLCLSGFQA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LDVPPPAGPFWILGDVFLGTYVAVFDRGDMKSSARVGLARARTRGADLGWGETAQAQFPG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 PGDKPIFVPLSNYRDVQYFGEIGLGTPPQNFTVAFDIGSSNLWVPSRRCHFFSVPCWLHH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PGDKPIFVPLSNYRDVQYFGEIGLGTPPQNFTVAFDTGSSNLWVPSRRCHFFSVPCWLHH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MSPPPLLQPLLLLLPLLNVEPSGATLIRIPLHRVQPGRRTINLLRGWREPAELPKLGAPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 AAIGGIPLIAGEYIILCSEIPKLPAVSFLLGGVWFNLTAHDYVIQTTRNGVRLCLSGFQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LDVPPPAGPFWILGDVFLGTYVAVFDRGDMKSSARVGLARARTRGADLGWGETAQAQFPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AHFDGILGLGFPILSVEGVRPPMDVLVEQGLLDKPVFSFYLNRDPEEPDGGELVLGGSDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RFDPKASSSFQANGTKFAIQYGTGRVDGILSEDKLTIGGIKGASVIFGEALWEPSLVFAF
                                                                                                                                                                                                                                                                                                                                                                                                           1 MSPPPLLQPLLLLLLPLLNVEPSGATLIRIPLHRVQPGRRTLNLLRGWREPAELPKLGAPS
                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                   DB 12; Length 420;
                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/10180719;
Publication No. US20030166246A1
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
Hillman, Jennifer L.
Yue, Henry
Guegler, Karl J.
Corley, Neil C.
Shah, Purvi
TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                 100.0%; Score 2238; DB 12;
100.0%; Pred. No. 1.9e-209;
cive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Incyte Pharmaceuticals, Inc
                                                                                                                                                                                                                                             SEQUENCE DESCRIPTION: SEQ ID NO: 4 :
                                                                        LENGTH: 420 amino acida
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Porter Dr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
       TELEFAX: 650-845-4166
                           INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                              LIBRARY: LUNGAST01
CLONE: 877617
                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0
Marches 420; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 3174 Por
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                          IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: CA COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 2
US-10-180-719-4
                                                                                                                                                                                                                                                                         US-09-968-415-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361
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240 300

240

120

9

Gaps

240 253

180

313

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AHYIPPLIFVPVTVPAYWQIHMERVKVGPGLTLCAKGCAAILDIGISLIIGPTEEIRALH 300
                                                                                                                                                                                                                                                      301 AAIGGIPLIAGEYIILCSEIPKLPAVSFILGGVWFNLTAHDYVIQTTRNGVRLCLSGFQA 360
                                                                                                                                                                                                                                                                             RFDPKASSSFQANGTKFAIQYGTGRVDGILSEDKLTIGGIKGASVIFGBALWEPSLVFAF
                                                                                             AHFDGILGLGFPILSVEGVRPPMDVLVEQGLLDKPVFSFYLNRDPEEPDGGELVLGGSDP
                                                                                                                                                                                                                                                                                                                                   361 LDVPPPAGPFWILGDVFLGTYVAVFDRGDMKSSARVGLARARTRGADLGWGETAQAQFPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: TWO NOVEL HUMAN CATHESPIN PROTEINS NUMBER OF SEQUENCES: 4
CORRESPONDENCES: ADDRESS: ADDRESSE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPUTER: THE COMPATIBLE
COMPUTER: THE COMPATIBLE
COMPATIBLE SYSTEM: DOS
SOFTHARE: PRESENT OFFRICAL
APPLICATION NUMBER: US/10/094,080
FILING DATE: 07-MR-2002
CLASSIFICATION NUMBER: 09/387,413
APPLICATION NUMBER: 09/387,413
FILING DATE: cUnchnown>
ATTORNEY/AGENT INFORMATION:
NAME: BILLINGS, LUGY J
REGISTRATION NUMBER: 36,749
REFERENCE/OCKET NUMBER: PF-0125 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/10094080; Publication No. US20020187140A1; GENERAL INFORMATION: APPLICANT: Bandman, Olga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 395 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELER: 415-845-4166
TELEX: <Unknown>
INFOFMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIBRARY: LUNGNOT02
CLONE: 312099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.
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US-10-094-080-3
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Fatent No. US20020174446A1

GENERAL INFORMATION:

APPLICANT: Cohen, Dalia et al.

TITLE OF INVENTION: Identification of Genes Involved in

TITLE DE INVENTION: Alzheimer's Disease Using Drosophila Melanogaster:

TILE DE INVENTION NUMBER: 00/1-09-27

PRIOR PILING DATE: 2000-09-29

PRIOR PILING DATE: 2000-09-29

PRIOR FILING DATE: 2001-06-14

NUMBER OF SEQ ID NOS: 53

SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                Score 2232; DB 14;
Pred. No. 7.3e-209;
0; Mismatches 1;
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99.8%; Pred. No. 7.6e-209;
ive 0; Mismatches 1;
                                                                                                                    99.7%;
99.8%;
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Matches 419; Conservative
                                                                                                                  Query Match
Best Local Similarity 99.8
Matches 419; Conservative
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ORGANISM: Homo Sapien
                                     TYPE: PRT
ORGANISM: Homo Sapien
                                                                             US-10-288-222A-30
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US-09-964-899-11
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                    LENGTH: 420
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SEQ ID NO 30
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                                     259
YGTGRVHGILSEDKLTIGGIKGASVIFGELSGTQPGL--RFCPFDGILGLGFPILSVEGV 169
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Factor No. US20020064855A1
GENERAL INPORMATION:
FAPPLICANT: Lemischka, Ihor
APPLICANT: Lemischka, Ihor
TITLE OF INVENTION: GENES THAT REGULATE HEMATOPIETIC BLOOD FORMING STEM
TITLE OF INVENTION: CELLS AND USES THEREOF
TITLE OF INVENTION: CELLS AND USES THEREOF
TITLE OF INVENTION: US. 09/09/789,919
CURRENT APPLICATION NUMBER: US/09/789,919
CURRENT FILING DATE: 2001-02-21
NUMBER OF SEQ ID NOS: 96
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 44
                                                                                                                                          230 IHMERVKVGPGLTLCAKGCAAILDTGTSLITGPTEETRALHAAIGGIPLLAGEYIILCSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 NPSFVPLSKFMNTQYFGTIGLGTPPQNFTVVFDTGSSNLWVPSTRCHFFSLACWFHHRFN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 170 RPPMDVLVEQGLLDXPVPSFYLNRDPBEPDGGELVLGGSDPAHYIPPLTFVPVTVPAYWQ
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                                     200 RPPMDVLVEQGLLDKPVFSFYLNRDPEEPDGGELVLGGSDPAHYIPPLTFVPVTVPAYWQ
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COGGANISM: Mus musculus
US-09-789-919-44
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; Publication No. US20020192749A1
; GENERAL INFORMATION:
    APPLICANT: Moore, et al.
    TITLE OF INVENTION: Human Gene Polynucleotides, Polypeptides, and Antibodies
    TILE REPERENCE: PROS5P1
; CURRENT APPLICATION NUMBER: US/09/969,384
; CURRENT FILING DATE: 2001-10-03
; PRIOR PILING DATE: 2001-04-02
; PRIOR PILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/194,118
; PRIOR FILING DATE: 2000-09-03
; PRIOR PILING DATE: 2000-04-03
; RUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.0
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                                                                                                               1 MSPPPLLOPLLLLPLLNVEPSGATLIRIPLHRVOPGRRTLNLLRGWREPARLPKLGAPS
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                                     92.5%; Score 2069.5; DB 13; Length 395; 93.8%; Pred. No. 4.8e-193; ive 0; Mismatches 1; Indels 25;
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Pred. No. 3.1e-157;
7; Mismatches 15;
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                                       Query Match 92.5
Best Local Similarity 93.8
Matches 394; Conservative
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US-09-969-384-15
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LENGTH: 390
   US-10-094-080-3
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Best Local S:
Matches 334
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, LOCATION: (231)
, OTHER: INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-833-245-1469
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                        Score 1328; DB 11;
Pred. No. 6.2e-121;
0; Mismatches 6;
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GENERAL INCRATION:
ITILE OF INVENTION: 17 Human Secreted Proteins
FILE REFERENCE: PS72391
CURRENT APPLICATION NUMBER: US/10/277,802
CURRENT FILING DATE: 2002-10-23
FRIOR APPLICATION NUMBER: 09/915,582
PRIOR FILING DATE: 2001-07-27
FRIOR APPLICATION NUMBER: PCT/US01/01431
PRIOR FILING DATE: 2001-01-7
PRIOR FILING DATE: 2001-01-7
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-04
FRIOR FILING DATE: 2000-02-04
FRIOR FILING DATE: 2000-09-12
NUMBER OF SEQ ID NOS: 97
SOFTWARE: PATCHTIN VET. 2.0
SEQ ID NO 66
LENGTH: 262
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Publication No. US20030190707A1
GENERAL INFORMATION:
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Best Local Similarity 97.6%;
Matches 249; Conservative
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PRIOR FILING DATE: 2000-04-25
                     NUMBER OF SEQ ID NOS: 2267
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1469
LENGTH: 262
                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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NAME/KEY: SITE
                                                                                                                                                                                                          NAME/KEY: SITE
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                                                                                                             Sequence 66, Application US/09915582
Fatent No. US2020120103A1
GENERAL INFORMATION:
TITLE OF INVENTION: 17 Human Secreted Proteins
FILE REFERENCE: PS723P1
CURRENT APPLICATION NUMBER: US/09/915,582
CURRENT FILING DATE: 2001-07-27
FRIOR APPLICATION NUMBER: 60/179,065
FRIOR PELLING DATE: 2000-01-31
FRIOR FILING DATE: 2000-01-31
FRIOR FILING DATE: 2000-03-34
FRIOR FILING DATE: 2000-03-34
FRIOR FILING DATE: 2000-03-34
FRIOR FILING DATE: 2000-03-34
FRIOR FILING DATE: 2000-03-34
FRIOR APPLICATION NUMBER: 60/130,68
FRIOR APPLICATION NUMBER: 60/231,968
FRIOR FILING DATE: 2000-03-12
NUMBER OF SEQ ID NOS: 97
SEQ ID NO 66
LENGTH: 262
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Publication No. US20040010134A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFRENCE: PFS46PCT
CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-12-21
PRIOR PLING DATE: 2000-13-21
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US-09-833-245-1469
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RESULT 13
US-09-915-582-87
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MSPPPLLQPLLLLLPLLNVEPSGATLIRIPLHRVQPGRRTLNLLRGWREPAELPKLGAPS
                                                           PGDKPIFVPLSNYRDVQYFGEIGLGTPPQNFTVAFDTGSSNLWVPSRRCHFFSVPCWLHH
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Sequence 670, Application US/09925302;
Patent No. US20020044941A1;
GENERAL INFORMATION:
APPLICANT: ROSE at al.;
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies;
FILE REFERENCE: PA104;
CURRENT APPLICATION NUMBER: US/09/925,302;
CURRENT FILING DATE: 2001-08-10;
PRIOR PLING DATE: 2000-03-08;
PRIOR FILING DATE: 1999-03-12;
NUMBER OF SEQ ID NOS: 896;
SOFTWARE: PatentIn Ver. 2.0;
SEQ ID NO 670
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Pred. No. 2.4e-106;
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al Similarity 80.7%;
230; Conservative
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 230; Conserv
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; Sequence 670, Application US/09925302 ; Publication No. US20030064072A9

RESULT 12 US-09-925-302-670

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 PSGATLIRIPLHRVQPGRRTLNLLRGWREPAELPKLGAPSPGDKPIFVPLSNYRDVQYPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43 PSGATLIRIPLHRVQPGRRILNLLRGWREPAELPKLGAPSPEDKPIFVPLSNYKG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42;
                                                                                                                                                                                                                                                                                                                                                                                                                          Length 285;
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REPERENCE: PA104
CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: CT/US00/05918
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 896
SOFTWARE: PATON NOWER: 2.0
SEQ ID NO 670
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1179; DB 12;
Pred. No. 2.4e-106;
4; Mismatches 9;
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Patent No. US20020120103A1

GENERAL INFORMATION:
TILE OF INVENTION: 17 Human Secreted Proteins
FILE REFERENCE: PS723P1

CURRENT APPLICATION NUMBER: US/09/915,582

CURRENT FILING DATE: 2001-07-7

PRIOR FILING DATE: 2001-01-7

PRIOR PILING DATE: 2000-01-31

PRIOR PILING DATE: 2000-02-04

PRIOR PILING DATE: 2000-02-04

PRIOR PILING DATE: 2000-09-12

NUMBER OF SEQ ID NOS: 97

SOFTWARE: PATENTIN VET: 2.0
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Best Local Similarity 80.7%;
Matches 230; Conservative
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CORGANISM: Homo sapiens
US-09-925-302-670
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LOCATION: (9)
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RESULT 15
US-10-277-802-87
; Sequence 87, Application US/10277802
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-833-245-1471
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                                                                                                                                                                                              76 TGTSLITGPTEEIRALHAAIGGIPULAGEYIILCSEIPKLPAVSFLLGGVWFNLTAHDYV 135
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                                                                                                        DPEEPDGGELVIGGSDPAHYIPPLTFVPVTVPAYWQIHMERVKVGPGLTLCAKGCAAILD 75
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Best Local Similarity 100.0%; Pred. No. 6.2e-94;
Matches 197; Conservative 0; Mismatches 0; Indels 0
    46.9%; Score 1050; DB 9; Length 212; 100.0%; Pred. No. 6.2e-94; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1471, Application US/0983245
Publication No. US20040010134A1
GENERAL INFORMATION:
APULICANT: Human Genome Sciences, Inc.
ITILE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF546FOT
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR APPLICATION NUMBER: 60/226, 931
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR APPLICATION NUMBER: 60/199, 384
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/199, 384
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
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Query Match
Best Local Similarity 100.0
Matches 197; Conservative
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ORGANISM: Homo sapiens
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LENGTH: 212
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; LOCATION: (9); ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-10-277-802-87
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100.0%; Pred. No. 6.2e-94;
iive 0; Mismatches 0;
                                                 GREKAL INCRMALIOUS:
GREKAL INCRMALIOUS:
TITLE OF INVENTION: 17 Human Secreted Proteins
FILE REPERENCE: P5723P1
CURRENT APPLICATION NUMBER: US/10/277,802
CURRENT FILING DATE: 2002-10-23
FRICR APPLICATION NUMBER: 09/915,582
FRICR APPLICATION NUMBER: 00/915,682
FRICR APPLICATION NUMBER: PCT/US01/01431
FRICR APPLICATION NUMBER: 60/179,065
FRICR APPLICATION NUMBER: 60/179,065
FRICR FILING DATE: 2000-01-31
FRICR APPLICATION NUMBER: 60/139,968
FRICR FILING DATE: 2000-01-31
FRICR APPLICATION NUMBER: 60/231,968
FRICR FILING DATE: 2000-09-12
FRICR FILING DATE: 2000-09-12
FRICR FILING DATE: 2000-09-12
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Job time : 75.8784 secs
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Publication No. US20030190707A1 GENERAL INFORMATION:
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Matches 197; Conservative
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RESULT 1
US-09-008-271A-4
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Sequence 3, Al
Sequence 3, Al
Sequence 10,
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Sequence 4, A
Sequence 12,
                                                                                                                      1 MSPPPLLQPLLLLLLPLLNVE.....ARTRGADLGWGETAQAQFPG 420
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Sequence 6,
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                                                         June 2, 2004, 20:16:40 ; Search time 29.2707 Seconds
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   /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-705-448-1
US-09-705-448-1
US-08-72-938-3
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US-09-387-413-3
US-09-387-413-3
US-09-387-48-10
US-08-974-691-3
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US-08-974-691-4
US-08-974-691-4
US-08-974-691-4
US-08-915-095A-12
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US-08-798-096-13
US-08-798-095A-13
US-09-953-956-13
US-08-553-125A-13
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Maximum Match 100%
Listing first 45 summaries
                                      - protein search, using sw model
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Gapop 10.0 , Gapext
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2238
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Match Length
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1877
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Maximum DB
                                     OM protein
                                                                                                                       Sequence:
                                                                                                                                                                        Searched:
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                                                          Run on:
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No.
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Sequence 2,
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Hillman, Jennifer L.
Yue, Henry
Guegler, Karl J.
Corley, Neil C.
Tang, Tom Y.
Shah, Purvi
TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS.
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPOTER: IBM Compatible
OPERATING SYSTEM: DOS
SOSTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/008,271A.
FILING DATE: 16-Jan-1998
PRICATION NUMBER: <UNKNOWN>
FILING DATE: <UNKNOWN>
ATORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 41,201
REGISTRATION NUMBER: 41,201
REFERENCE/DOCKET NUMBER: PF-0458 US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
US-09-802-633-9
US-01-114-464-13
US-09-215-450-23
US-09-215-450-23
US-09-215-450-23
US-09-604-668-31
US-09-603-523-3
US-08-328-314-2
US-08-328-314-2
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US-08-328-314-2
US-08-368-36-24
US-08-368-36-24
US-08-68-68-32-24
US-08-088-633-2
US-08-088-633-2
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US-08-441-751-2
                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LUNGASTO1
CLONE: 877617
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                            Sequence 4, Application US/09008271A Patent No. 6203979 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 420 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
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STATE: CA
COUNTRY: USA
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240 240 300 300

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AAIGGIPLLAGEYIILCSEIPKLPAVSFLLGGVWFNLTAHDYVIQTTRNGVRLCLSGFQA 360
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61 PGDKPIFVPLSNYRDVQYFGEIGLGTPPQNFTVAFDTGSSNLWVPSRRCHFFSVPCWLHH 120
                                                                                                                                                          181 AHFDGILGLGFPILSVEGVRPPMDVLVEQGLLDKPVFSFYLNRDPEEPDGGELVLGGSDP
                                                                                                                                                                                                                                       241 AHYIPPLTFVPVTVPAYWQIHMBRVKVGPGLTLCAKGCAAILDTGTSLITGPTBEIRALH
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                                            121 RFDPKASSSFQANGTKFALQYGTGRVDGILSEDKLTIGGIKGASVIFGEALWEPSLVFAF
                                                                                                                          181 AHFDGILGLGFPILSVEGVRPPMDVLVEQGLLDKPVFSFYLNRDPEEFDGGELVLGGSDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/08974691
; Patent No. 6225103
; GENERAL INFORMATION:
; GENERAL INFORMATION:
; APPLICANT: Lin, Xinli
; APPLICANT: Tang, Jordan
; TITLE OF INVENTION: Cloning and Characterization of Napsin
; NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center, 1201 W. Peachtree
STREET: St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCEPTION NUMBER: US/08/974,691
PILING DATE: 20-NOV-1997
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/031,196
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/046,126
PRIOR APPLICATION NUMBER: US 60/046,126
FILING DATE: 09-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
NAME: Pabst, Patrea L.
REFERENCE/DOCKET NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMER 166
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO:
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MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS: ADDRESSE: Patrea L.
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STATE: GA
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US-08-974-691-8
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                       Length 420;
                                                                  Indels
                       100.0%; Score 2238; DB 3;
100.0%; Pred. No. 2e-222;
ive 0; Mismatches 0;
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Patent No. 6432690
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: With Hong
APPLICANT: Bruno, Sandra A.
APPLICANT: Elsenboss, Laura A.
APPLICANT: Cohan, Victoria L.
APPLICANT: Bandman, Olga
ITLE OF INVENTION: HUMAN ASPARTIC PROTEASES
FILE REFERENCE: PF-0458-1 CIP
CURRENT APPLICATION NUMBER: US/09/705,448
CURRENT FILING DATE: 1998-07-16
FRIOR APPLICATION NUMBER: 09/116,641
PRIOR FILING DATE: 1998-07-16
FRIOR FILING DATE: 1998-07-16
FRIOR FILING DATE: 1998-01-16
NUMBER OF SEQ ID NOS: 10
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US-09-705-448-1
                                                                  Matches 420; Conservative
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                                               Similarity
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LENGTH: 420
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US-09-705-448-1
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                       Query Match
Best Local
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                                                                                                                                                                                                                                                                                               25;
                                                                                                                                                                                                                                                 Score 2069.5; DB 1; Length 395;
Pred. No. 4.6e-205;
0; Mismatches 1; Indels 25;
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APPLICANT: Coleman, Roger
TITLE OF INVENTION: TWO NOVEL HUMAN CATHESPIN PROTEINS
NUMBERS OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,538
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/723,938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/09080538; Patent No. 5965129
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SYSTEM: DOS
FastSEQ Version
                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 93.8%;
Matches 394; Conservative
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MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                         N-terminal
STRANDEDNESS: single
TOPOLOGY: linear
                   TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                               ANTI-SENSE: NO
FRAGMENT TYPE: N-termi
ORIGINAL SOURCE:
IMMEDIATE SOURCE:
LIBRARY: LUNONOTO2
CLONE: 312099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM COM
OPERATING SYSTEM:
SOFTWARE: FastSEQ
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                                                                                                                  1 MSPPPLLQPLLLLLPLLNVEPSGATLIRIPLHRVQPGRRILNLLRGWREPAELPKLGAPS
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      Length 420
                                           Indels
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GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Coleman, Roger
APPLICANT: Coleman, Roger
TWO NOVEL HUMAN CATHESPIN PROTEINS
  Score 2232; DB 3;
Pred. No. 8.5e-222;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Incyte Pharmaceuticals, Inc. 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF-0125 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FASTERQ VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/723,938
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/08723938
Patent No. 5776759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
99.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 395 amino acids
                                              Matches 419; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVESTIGES: TWO WHERE OF SEQUENCES: TWO CORRESPONDENCE ADDRESS: ADDRESSE: Incyte Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Palo Alto
STATE: CA
                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-723-938-3
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    Query Match
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SEQUENCE CHARACTERISTICS:
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ZIP: 94304
COMPUTER READABLE FORM:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMMEDIATE SOURCE
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US-08-974-691-6
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                                                                                                                                                                                                                                                                                                                                                                                                                             Length 395;
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CORRESPONDENCES: ADDRESS: ADDRESSEE: INOYTE Pharmaceuticals, Inc. STREET: 3174 Porter Drive STREET: ADA ALTO STATE: CA COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                         92.5%; Score 2069.5; DB 2
93.8%; Pred. No. 4.6e-205;
live 0; Mismatches 1;
                                                                  PF-0125 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/09387413
Patent No. 6475483
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
                              NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
                                                            REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
                                                                                                                                               INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 395 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 394; Conservative
                                                                                                                                                                                                                                                                                                                                       ; IMMEDIATE SOURCE:
; LIBRARY: LUNGNOT02
; CLONE: 312099
US-09-080-538-3
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
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Best Local Similarity 93.8%; Pred. No. 4.6e-205;
Matches 394; Conservative 0; Mismatches 1;
                                                                                                                                       APPLICATION NUMBER: US/09/387,413
FILING DATE: 31-Aug-1999
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: 09/080,538
FILING DATE: «Unknown»
ATTORNEY, AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLONE: 312099
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-SEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 395 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
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61 PGDKPASVPLSKFLDAQYFGEIGLGTPPQNFTVAFDTGSSNLWVPSRRCHFFSVPCWFHH 120
                                                                                                                       121 RFDPKASSSFQANGTKFAIQYGTGRVDGILSEDKLTIGGIKGASVIFGEALWEPSLVFAF 180
301 AAIGGIPLLAGEYIILCSEIPKLPAVSFLLGGVWFNLTAHDYVIQTTRNGVRLCLSGFQA 360
                        361 LDVPPPAGPFWILGDVFLGTYVAVFDRGDMKSSARVGLARARTRGADLGWGETAQAQFPG 420
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Patent No. 6225103
GENERAL INFORMATION:
APPLICANT: Keolsch, Gerald
APPLICANT: Lin, Xinli
APPLICANT: Tang, Jordan
TITLE OF INVENTION: Cloning and Characterization of Napsin
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 451;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center, 1201 W. Peachtree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,691
FILING DATE: 20-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 84.8%; Score 1897; DB 3;
Best Local Similarity 86.0%; Pred. No. 3.6e-187;
Matcher 361; Conservative 16; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRICR APPLICATION:
PRICR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 20-NOV-1996
PRICR APPLICATION NUMBER: US 60/046,126
FILING DATE: 09-NAY-1997
ATTCRNEY/AGENT INFORMATION:
NAME: Paber, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: 31,284
TELECHONE: 404-873-8794
TELECHONE: 404-873-8794
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TYPE: amino acid
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US-08-974-691-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein ORIGINAL SOURCE:
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TCPOLOGY: lin
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                                                                                                                                                                                                               RESULT 8
US-08-974-691-2
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                                          GENERAL INFORMATION:
APPLICANT: Keolsch, Gerald
APPLICANT: Lin, Xinli
APPLICANT: Tang, Jordan
TITLE OF INVENTION: Cloning and Characterization of Napsin
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center, 1201 W. Peachtree
                                                                                                                                                                                                                                     2800 One Atlantic Center, 1201 W. Peachtree St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PLICATION WIMBR: US/08/974,691
FILING DATE: 20-NOV-1997
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APPLICATION NUMBER: US 60/031,196
FILING DATE: 20-NOV-1996
FRICH APPLICATION DATA:
APPLICATION NUMBER: US 60/046,126
FILING DATE: 09-MAY-1997
ATTONEY/AGBNT INFORMATION:
NAME: Pabst, Patrea L.
REGISTATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: 0MRF 166
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 6:
SEQUENCE CHARACTER SIGHTS:
SEQUENCE CHARACTER SIGHTS:
SEQUENCE CHARACTER SIGHTS:
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                                                                                                                                                                                                                                                                                                         STATE: GA
COUNTY: USA
ZIP: 30309-3450
ZIP: 30409-3450
COMPUTER READABLE FORM:
REDLUM TYPE: FLODBY disk
COMPUTER: IBM PC COMPALILLE
OPERATING SYSTEM: PC-DOS/MS-D
6, Application US/08974691
3. 6225103
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Matches 361; Conservative
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STRANDEDNESS: single
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ORIGINAL SOURCE:
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  Sequence 6,
Patent No.
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59 NPSFVPLSKFWNTQYRGTIGLGTPPQNFTVVFDTGSSNLWVPSTRCHFFSLACWFHHRFN 118
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                                                                                                                          420
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                                                                   301 AAIGGIPLLAGEYIILCSEIPKLPAVSFLLGGVWFNLTAHDYVIQTTRNGVRLCLSGFQA
                                                                                                                          361 LDVPPPAGPFWILGDVFLGTYVAVFDRGDMKSSARVGLARARTRGADLGWGFTAQAQFPG
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                                                                                                                                                                                                                                                                                                                                   APPLICANT: Keolsch, Gerald
APPLICANT: Lin, Xinli
APPLICANT: Tang, Jordan
TITLE OF INVENTION: Cloning and Characterization of Napsin
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
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STREET: 2800 One Atlantic Center, 1201 W. Peachtree
STREET: St.
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,691
FILING DATE: 20-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 69.9%; Score 1564.5; DB 3;
Best Local Similarity 70.5%; Pred. No. 6.8e-153;
Matches 297; Conservative 36; Mismatches 79;
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PILING DATE: 09-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Pabet, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMFF 166
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-873-8794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 20-NOV-1997
CLASSTRICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/031,196
FILING DATE: 20-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/046,126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                     Sequence 3, Application US/08974691; Patent No. 6225103; GENERAL INFORMATION:
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STATE: GA
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                                                                                             SRPDGIIGIGFPILSVEGVRPPLDVLVEQGLLDKPVFSFYFNRDPEVADGGELVLGGSDP 240
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                                                                                                                                                                                         241 AHYIPPLIFVPVIVPAYWQIHMERVKVGSRLTLCAQGCAAILDIGIPVIVGPTEIRALH 300
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    1 MSPPPLLQPLLLLLPLLNVEPSGATLIRIPLHRVQPGRRTLNLLRGWREPAELPKLGAPS
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                                                                 AHFDGILGLGFPILSVEGVRPPMDVLVEQGLLDKPVFSFYLNRDPERPDGGELVLGGSDP
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al Similarity 85.2%; Pred. No. 4e-185;
358; Conservative 17; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Xu, Hong
APPLICANT: Bruno, Sandra A.
APPLICANT: Bruno, Sandra A.
APPLICANT: Brenboss, Laura A.
APPLICANT: Togliano, Michael
APPLICANT: Cohan, Victoria L.
APPLICANT: Gohan, Victoria L.
APPLICANT: Bandman, Olga
TITLE OF INVENTION: HUMAN ASPARTIC PROTEASES
FILE REFRENCE: PF-0458-1 CIP
CURRENT APPLICATION NUMBER: US/09/705,448
CURRENT APPLICATION NUMBER: 09/116,641
PRIOR FILING DATE: 1998-07-16
PRIOR APPLICATION NUMBER: 09/008,271
PRIOR FILING DATE: 1998-01-16
NUMBER OF SEQ ID NOS: 10
SOFFWARE: FastSEQ for Windows Version 3.0
SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION: 322
; OTHER INFORMATION: 2435410, EOSINOT03
US-09-705-448-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/09705448
Patent No. 6432690
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    244 IPPLTFVPVTVPAYWQIHMERVKVGPGLTLCAKGCAAILDTGTSLITGPTEEIRALHAAI 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                     359 PKPAGPLWILGDVFLGPYVAVFDRGDKNVGPRVGLARAQSRS/TDRAERR/TYQAQFFKRRP
                                                                                                                                                                                             304 GGIPLLAGEYIILCSEIPKLPAVSFLLGGWWFNLTAHDYVIQTTRNGVRLCLSGFQALDV
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                                                          S39 VPPLTFIPVTIPAYWOVHMESVKVGTGLSLCAQGCSAILDTGTSLITGPSEEIRALNKAI
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Patent No. 5501969;
GENERAL INFORMATION:
TITLE OF INVENTION: Human Osteoclast-Derived Cathepein;
TORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: ROSSELAND
CITY: ROSSELAND
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45.4%; Score 1015; DB 1;
Best Local Similarity 46.9%; Pred. No. 3.5e-96;
Matches 196; Conservative 71; Mismatches 125;
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PRICR APPLICATION DATA:
APPLICATION NUMBER: 0.5501969e
FILING DATE: No.5501969e
ATTCRNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 35.134
REFERENCE/DOCKET NUMBER: 325800-95
TELECHONE: 201-994-1700
TELECHONE: 201-994-1744
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/25 INCH DISKETTE
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
FILING DATE: MS-COMPUTE: MS-COMP
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TYPE: AMINO ACID
STRANDEDNESS:
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LENGTH: 412 AMINO ACID
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US-08-208-007A-12
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                                                                                                                                                                                                                                                                                                                                                                                     339 VPPLTFIPVTIPAYMQVHMESVKVGTGLSLCAQGCSAILDTGTSLITGPSEEIRALNKAI 298
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304 GGIPLLAGEYIILCSEIPKLPAVSFLLGGVWFNLTAHDYVIQTTRNGVRLCLSGFQALDV 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      364 PPPAGPFWILGDVFLGTYVAVFDRGDMKSSARVGLARARTRGADLGWGETAQAQF----P 419
                                                                                                                                                                                                                                                                                                                               244 IPPLTFVPVTVPAYWQIHMERVKVGPGLTLCAKGCAAILDTGTSLITGPTEEIRALHAAI 303
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APPLICANT: Bruno, Sandra A.
APPLICANT: Brenno, Sandra A.
APPLICANT: Brennos, Laura A.
APPLICANT: Brennos, Laura A.
APPLICANT: Cohan, Victoria L.
APPLICANT: Bandman, Olga
TITLE OF INVENTION: HUMAN ASPATIC PROTEASES
FILE OF INVENTION: HUMAN ASPATIC PROTEASES
FILE OF INVENTION: HUMBER: US/09/705,448
CURRENT APPLICATION NUMBER: US/0116,641
PRIOR FILING DATE: 1998-07-16
PRIOR FILING DATE: 1998-07-16
PRIOR FILING DATE: 1998-07-16
PRIOR FILING DATE: 1998-01-16
NUMBER: OF SEQ ID NOS: 10
SOSTWARE: FREEEQ for Windows Version 3.0
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US-09-705-448-10
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ORGANISM: MUS MUSCULUS
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US-09-705-448-10
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-GGIKGA 163
                                                                                                                                                                                                                                                         356 LKVSQAGKTLCLSGFMGMDIPPPSGGPLWILGDVFIGRYYTVFDR----DNNRVGFAEA 409
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                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Keolsch, Gerald
APPLICANT: Lin, Xinli
APPLICANT: Tang, Jordan
TITLE OF INVENTION: Cloning and Characterization of Napsin
WUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5: Patrea L. Pabst
2800 One Atlantic Center, 1201 W. Peachtree
115 PCWLHHRFDPKASSSFQANGTKFAIQYGTGRVDGILSEDKLTI-
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILLING DATE: 20-NOV-1997
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APPLICATION NUMBER: US 60/031,196
FILING DATE: 20-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/046,126
FILING DATE: 09-MAY-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/08974691 Patent No. 6225103 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-873-8794
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 412 amino acid
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MOLECULE TYPE: protein
ORIGINAL SOURCE:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STRANDEDNESS: si
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STATE: GA
COUNTRY: USA
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CLASSIFICATION:
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APPLICANT: Hastings, et al.; TITLE OF INVENTION: HUMAN OSTEOCLAST-DERIVED CATHEPSIN; FILE REFERENCE: PF10704; CURRENT APPLICATION NUMBER: US/08/915,095A; CURRENT FILING DATE: 1997-08-20; NUMBER OF SEQ ID NOS: 14; SOFTWARE: Patentin Ver. 2.1; SEQ ID NO 12
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                                                     Indels
46.9%; Pred. No. 3.5e-96;
tive 71; Mismatches 125;
     Local Similarity 46.9% nes 196; Conservative
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296 TGTSLMVGPVDEVRELQKAIGAVPLIQGEYMIPCEKVSTLPAITLKLGGKGYKLSPEDYT 355
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284 TGTSLITGPTEEIRALHAAIGGIPLLAGEYIILCSEIPKLPAVSFLLGGVWFNLTAHDYV 343
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                                                                                     344 IQTTRNGVRLCLSGFQALDVPPPAGPFWILGDVFLGTYVAVFDRGDMKSSARVGLARA 401
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                                                                                                                                                                                 Sequence 12, Application US/08798096
Patent No. 6387682.

Patent No. 6387682.

APPLICANT: Hastings, et al.

TITLE OF INVENTION: HUMAN OSTEOCLAST-DERIVED CATHEPSIN CURRENT APPLICATION NUMBER: US/08/798,096

CURRENT FILING DATE: 1997-02-12

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                    RESULT 15
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Gen Copyright (c)	protein search, using	June 2, 2004, 19	US-09-700-770-8 2238 1 MSPPPLLQPLLLLLPLLNVE	BLOSUM62 Gapop 10.0 , Gapext	1586107 segs, 28	hits satisfying	length: 0 length: 2000000000	Minimum Match Maximum Match Listing first	A_Geneseq_29Jan04:: 1: geneseqp1990s:* 2: geneseqp1990s:* 3: geneseqp2000s:* 4: geneseqp2001s:* 5: geneseqp2003s:* 7: geneseqp2003ss: 8: geneseqp2003bs:	is the number of : ter than or equal ived by analysis	ж	Query Match Length DB	100.0 420 2 100.0 420 3	44	420 433	395 438	451	390	44 9	288	262	262 285	212	212	410	410
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Human	Human	Aar74207 Human dea	Aaw71369 Death ass	Aay06478 Human tum	Aay93685 Amino aci	Aau72879 Human asp	Abb58237 Drosophil	Aag63965 Amino aci	Abr48169 Human bla	Abu56634 Lung canc	Aae01696 Human gen	Human	Ada57490 Human sec	Ada41368 Human sec	Abr48085 Human sec	Adc74513 Human sec	Aag75543 Human col	Aam23663 Human EST	Abb07483 Theobroma
ABR47867	ADC74257	AAR74207	AAW71369	AAY06478	AAY93685	AAU72879	ABB58237	AAG63965	ABR48169	ABU56634	AAE01696	ABG63960	ADA57490	ADA41368	ABR48085	ADC74513	AAG75543	AAM23663	ABB07483
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526	7.7	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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309
/note= "potential leucine zipper pattern start point"
316
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336
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283
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393
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                                                                                                                                                              Aspartic protease; human; HUPM-4; cell proliferation; cancer; immune disorder; inflammation; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "characteristic of aspartic protease"
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1. 21
1. 0.21
2. 1. 22
2. .420
Inote = "putative mature protein"
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                                 AAYC6435 standard; protein; 420 AA.
                                                                                                 (first entry)
                                                                                                                                  Human protease HUPM-4.
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Peptide
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Thu Jun

us-09-700-770-8.rag

(first entry)

AAY44809;

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Human; aspartic protease-1; NHAP-1; chromosome 19q13.3; antiallergic;
                                                         Human Aspartic Protease-1 (NHAP-1).
                            18-MAY-2000
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                                                                                                                                                                                                                                                                                                                 from the consensus sequence (see AAX81152) of overlapping cDNA clones obtained from various libraries. Northern analysis shows expression of HUPM-4 in cardiovascular, haematopoietic, and male and female reproductive cDNA libraries. Approximately 56% of these libraries are associated with neoplastic disorders, 18% with inflammation and the immune response, i.e. HUPM-1 to -12 (see AAX80432-43), and the polymortection provides 12 new human proteases, i.e. HUPM-1 to -12 (see AAX80432-43), and the polymortectides encoding them (see AAX87149-60). Also provided are vectors, host cells and methods for producing HUPM polypoptides, as well as agonists and antagonists of HUPM. Methods for preventing cell providerative disorders and immune disorders using HUPM or HUPM
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                                                                                                                                                                                                                            Novel human protease molecules useful in the treatment of developmental disorders and/or cancers.
                                                                                                                                                                                                                                                                                                       present sequence represents novel human protease HUPM-4, as deduced
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                                                                                                                                     Guegler KJ,
                                                                                                                                                                                                                                                                         Claim 1; Page 72-73; 90pp; English.
                                                                                                                                       Yue H,
                                              99WO-US000655,
                                                                            98US-00008271
                                                                                                        PHARM INC
                                                                                                                                     Hillman JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antagonists are claimed
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N-PSDB; AAX87152.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 420 AA;
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                                              12-JAN-1999;
                                                                          16-JAN-1998;
                   22-JUL-1999
                                                                                                                                     Bandman O,
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AAY44809 standard; protein; 420 AA

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New human aspartic protease polypeptide useful for treating and detecting
immunosuppressive, cytostatic, antiasthmatic, antinflammatory; cancer; antiatteriosclerctic; antithyroid, antibacterial, neuroprotective; antidiabetic; anti-HIV, osteopathic, antiarthritic; treatment; cretinism; endocrinological, hypopandism; Sheehan syndrome, diabetes insipidus; hypothyroidism; adenocarcinoma; leukaemia; immunological; amyloidosis; acquired immune defliciency syndrome; AIDS; Addison's disease; arthritis; osteoporosis; atheroselerosis; infection; respiratory; allergy; asthma; emplysema; gene therapy; diagnosis.
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/label= Mature_NHAP-1
/note= "Homologous to mouse aspartic protease-like
protein (GI 1906810)"
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/label= Signal_peptide
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N-FSDB; AAZ50231.
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12-MAY-1999;

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                                                                                The present sequence is human aspartic protease-1 (NHAP-1) encoded by cDNA obtained from human lung cDNA library. NHAP-1 gene is located on chromosome 19q13. NHAP has immunosuppressive, antialraptic, cytostatic, antiatesthmatic, antiinflammatory, antiatreriosclerotic, antithyroid, antibacterial, neuroprotective, antidiabetic, anti-HIV, osteopathic and antiatrhritic activity. It is useful for treating and preventing endocrinological disorders like hypogonadism, Sheehan syndrome, diabetes insipidus, cretinism and hypothyroidism, cancers like adenocarcinoma and leukaemia, immunological disorders like acquired immune deficiency atherosclerosis addison's disease, amyloidosis, arthritis, osteoporosis, atherosclerosis and microbial infections and respiratory disorders like allergy, asthma and emphysema. NHAP pollynucleotides can be used in gene therapy and for diagnosis of disorders associated with expression of NHAP
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 endocrinological disorders e.g. hypogonadism, Sheehan syndrome
                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 2238; DB 3; Length 420; 100.0%; Pred. No. 6.9e-203; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human lung specific gene protein Lng105
                                                    Disclosure; Fig 1; 83pp; English
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Matches 420; Conservative 0
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                                                                                                                                                                                                                                                                                                                                         Sequence 420 AA;
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PGDKPIFVPLSNYRDVQYFGEIGLGTPPQNFTVAFDTGSSNLWVPSRRCHFFSVPCWLHH 120
                                                                                                                                                                                                                   The present sequence is a lung specific gene (LSG) protein Lng105 from human clone ID 3107312. The LSG has high level of tissue specificity for lungs and is overexpressed in cancerous tissues. The sequence serves as a diagnostic marker for detecting, monitoring, staging and prognosticating lung cancer. The diagnosis involves comparing levels of LSG in samples obtained from patient and normal control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 AHYIPPLIFVPVTVPAYWQIHMERVKVGPGLTLCAKGCAAILDTGTSLITGPTEEIRALH 300
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                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                new method for diagnosing, monitoring and staging lung cancer
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Pred. No. 6.9e-203;
; Mismatches 0;
                                                                                                                                                                                           Example 2; Page 37-38; 40pp; English
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                                                          DIADEXUS LLC
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                                                                                      Macina RA,
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Matches 420;
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The invention relates to methods and compositions for treating a subject having a cardiovascular disorder using 139, 258, 1261, 1486, 2398, 2414, 7601, 8587, 10183, 10183, 10183, 10183, 10180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 170180, 17018
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Treating a subject having a cardiovascular disorder, e.g. angina, arrhythmia, or restenosis, comprises administering a 139, 258, 1261, 1486, 2398, 2414, 7660, 8587, 10183, 10550, 12680, 17921, 32248, 60489 or 93804 modulator.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MSPPPLLQPLLLLLPLLNVEPSGATLIRIPLHRVQPGRRTLNLLRGWREPAELPKLGAPS
restenosis; cardiac hypertrophy; ischaemia reperfusion injury; angina arteriosclerosis; coronary artery ligation; rheumatic heart disease; heart failure; hypertension; cardiomyopathy; myocardial infarction; arterial inflammation; microembolism; atherosclerosis; endocarditis; vascular heart disease; valvular disease; arrhythmia; gene therapy; sinus node dysfunction; napsin A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 420;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 2232; DB 6;
Pred. No. 2.6e-202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 123-124; 124pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Galvin KM;
                                                                                                                                                                                                                                                                                                                                    05-NOV-2002; 2002WO-US035538.
                                                                                                                                                                                                                                                                                                                                                                                  05-NOV-2001; 2001US-0339582P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2003-441437/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                       (MITT-) MITTENNIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Iocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chun M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAD56525.
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                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                               15-MAY-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Logan TJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents the human napsin B protein, encoded by the cDNA sequence given in AAV27038. The N-terminus of this cDNA was obtained by splicing together isolated napsin cDNA clones, which had been found by screening a human liver cDNA library, whereas the C-terminus was obtained by using genomic clones. Napsin B is an aspartic protease which was isolated from human liver
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                                                                                                                                                                                                                                                                                                                                                                                  from human liver - potentially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGDKPIFVPLSNYRDVQYFGEIGLGTPPQNFTVAFDTGSSNLWVPSRRCHFFSVPCWLHH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AHYIPPLTFVPVTVPAYWQIHMERVKVGPGLTLCAKGCAAILDTGTSLITGPTEEIRALH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAIGGIPLLAGEYIILCSEIPKLPAVSFLLGGVWFNLTAHDYVIQTTRNGVRLCLSGFQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAIGGIPLLAGEYIILCSEIPKLPAVSFLLGGVWFNLTAHDYVIQTTRNGVRLCLSGFQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AHYI PPLIFVPVTVPAYWQIHMERVKVGPGLTLCAKGCAAILDIGTSLITGPTEEIRALH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cardiovascular disorder; coronary artery disease; bradycardia;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 420;
                                                                                                                                                                                                                                                                                                                                                                                    isolated aspartic protease, napsin, from human l
ul for, e.g. diagnosis and treatment of disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99.7%; Score 2232; DB 2;
99.8%; Pred. No. 2.6e-202;
iive 0; Mismatches 1;
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                                                                                                                                                                                                       (OKLA-) OKLAHOMA MEDICAL RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 4; 24pp; English.
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                                                                                                                                                                                                                                                          Tang JJN;
                                                                             97WO-US021684.
                                                                                                                             96US-0031196P.
97US-0046126P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 99.8
Les 419; Conservative
                                                                                                                                                                                                                                                                                                          WPI; 1998-312482/27
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                                                                                                                                                                                                                                                          Lin X,
                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAV27038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 420
                                                                                                                                                     09-MAY-1997;
                                                                             20-NOV-1997;
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                                                                                                                                                       LDVPPPAGPFWILGDVFLGTYVAVFDRGDMKSSARVGLARARTRGADLGWGETAQAQFPG 420
181 AHFDGILGLGFPILSVEGVRPPMDVLVEQGLLDKPVFSFYLNRDPEFPDGGELVLGGSDP 240
                             AHYIPPLTFVPVTVPAYWQIHMERVKVGPGLTLCAKGCAAILDTGTSLITGPTEEIRALH 300
                                                 AAIGGIPLLAGEYIILCSEIPKLPAVSFLLGGVWFNLTAHDYVIQTTRNGVRLCLSGFQA 360
                                                                                                          301 AAIGGIPLLAGEYIILCSEIPKLPAVSFLLGGVWFNLTAHDYVIQTTRNGVRLCLSGFQA 360
                                                                                                                                                                      Neuroprotective; nootropic; transgenic fly; Alzheimer's disease; Abeta; amyloid precursor protein; tissue-specific expression control; human APP; APP pathway modulator; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New transgenic fly, containing DNA encoding an Abeta portion of human APP, useful for identifying agents which modulate the APP pathway and which can be used to treat Alzheimer's disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Konsolaki
                                                                                                                                                                                                                                                                                                                                                              Protein of NAP1 from aspartyl protease-related family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Finelli AL, Freuler F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NOVS ) NOVARTIS AG.
(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH
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                                                                                                                                                                                                                                                                AAO20497 standard; protein; 433
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14-JUN-2001; 2001US-0298309P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zusman S;
                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cohen D, Dengler UJ,
Reinhardt MWHM, Zusma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-315796/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAK99391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 433 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200226820-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                              27-JUN-2002
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                                                                                                                                                                                                                                                                                                 AAO20497;
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                                                                                                                                                                                                                                                 AA020497
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                                                                                                                                                133
                                                                                                                                                                                                                   193
                                                                                                                                                                                                                                                     181 AHFDGILGLGFPILSVEGVRPPMDVLVEQGLLDKPVFSFYLNRDPEEPDGGELVLGGSDP 240
                                                                                                                                                                                                                                                                        AHFDGILGLGFPILSVEGVRPPMDVLVEQGILDXFVFSFYLNRDPEEPDGGELVLGGSDP 253
                                                                                                                                                                                                                                                                                                                                             254 AHYIPPLTEVPVTVPAXWQIHMERVKVGPGLTLCAKGCAAILDTGTSLITGPTEBIRALH 313
                                                                                                                                                                                                                                                                                                                                                                                       301 AAIGGIPLLAGEYIILCSEIPKLPAVSFLLGGVWFNLTAHDYVIQTTRNGVRLCLSGFQA 360
                                                                                                                                                                                                                                                                                                                                                                                                              LDVPPPAGPFWILGDVFLGTYVAVFDRGDMKSSARVGLARARTRGADLGWGETAQAQFPG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          - useful
                                                                                                                                                                                                                                                                                                                    241 AHYIPPLIFVPVTVPAYWQIHMERVKVGPGLTLCAKGCAAILDIGTSLITGPTEEIRALH 300
                                                 9
                                                                           14 MSPPPLLQPLLLLLPLLNVEPSGATLIRIPLHRVQPGRRILNLLRGWREPAELPKLGAPS 73
                                                                                                                                                                                                       134 RFDPKASSSFQANGTKFAIQYGTGRVDGILSEDKLTIGGIKGASVIFGEALWEPSLVFAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human cathepsins and related nucleic acids, vectors and products - use for treatment and diagnosis of e.g. tumours, metastases, inflammation, neurological disease etc.
                                                                                                                  PGDKPIFVPLSNYRDVQYFGEIGLGTPPQNFTVAFDTGSSNLWVPSRRCHFFSVPCWLHH
                                                                                                                                              74 PGDKPIFVPLSNYRDVQYFGBIGLGTPPQNFTVAFDTGSSNLWVPSRRCHFFSVPCWLHH
                                                                                                                                                                                    RFDPKASSSFQANGTKFAIQYGTGRVDGILSEDKLTIGGIKGASVIFGEALWEPSLVFAF
                                             1 MSPPPLLQPLLLLLPLLNVEPSGATLIRIPLHRVQPGRRTLNLLRGWREPAELPKLGAPS
               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human cathepsin polypeptide-2; HCP-2; metastasis; antibody; agonist; antagonists; tumour; arthritis; Alzheimer's disease; HCP-1; Huntington's disease; mucolipidosis.
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               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amino acid sequence of human cathepsin polypeptide-2.
Pred. No. 2.7e-202;
; Mismatches 1;
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Local Similarity 99.8%;
nes 419; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Coleman R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-230698/20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-SEP-1996;
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                                                                                                                  61
                                                                                                                                                                                    121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          361
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LDVPPPAGPFWILGDVFLGTYVAVFDRGDMKSSARVGLARARTRGADLGWGETAQAQFPG 420
                                                                                                                                                                                                                                                                The present sequence represents a human aspartic protease. The present invention describes novel human aspartic proteases and also ESTs from human cDNA libraries having partial DNA sequences which encodes an aspartic protease. Compounds which inhibit aspartic protease, especially antibodies can be used in therapy where needed. The protease can also be used in therapy where needed. The protease can also be are the processing of endothelin and pro-opiomelanocortin prohomones. They may also be involved in the processing of serum amyloid A protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PGDKPASVPLSKFLDAQYFGEIGLGTPPQNFTVAFDTGSSNLWVPSRRCHFFSVPCWFHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PGDKPIFVPLSNYRDVQYFGEIGLGTPPQNFTVAFDTGSSNLMVPSRRCHFFSVPCWLHH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MSPPPLLQPLLLLLPLLNVEPSGATLIRIPLHRVQPGRRTLNLLRGWREPAELPKLGAPS
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                                                                                                                                                                                       Human aspartic protease and related DNA - which may be involved processing of endothelin and pro-opiomelanocortin pro-hormone(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                            84.8%; Score 1897; DB 2; Length 438;
86.0%; Pred. No. 1.4e-170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16; Mismatches
                                                                                                                                                                                                                                       Claim 14; Page 20; 32pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW54877 standard; protein; 451
                                                              PLC.
 97WO-GB002426.
                               96GB-00018966
                                                           SMITHKLINE BEECHAM
UNIV WALES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 86.03
Matches 361; Conservative
                                                                                                                                            1998-207396/18.
                                                                                                             Кау J,
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 438 AA;
                                                                                                                                                             N-PSDB; AAV28623
   09-SEP-1997;
                               11-SEP-1996;
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(UYWA-)
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                                                                                                                                                                                                          9
Alzheimer's and Huntington's diseases, and mucolipidosis. Fragments of HCP-2 are useful diagnostically (to detect or quantify gene expression), to monitor the effects of treatment and to map the corresponding genomic
                                                                                                                                                                                                   PGDKPI FVPLSNYRDVQYFGEIGLGTPPQNFTVAFDTGSSNLWVPSRRCHFFSVPCWLHH
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                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   endothelin; serum amyloid A protein;
                                                                                                                                              25;
                                                                                                              Length 395;
                                                                                                                                              Indels
                                                                                                           Score 2069.5; DB 2;
Pred. No. 5.6e-187;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW57042 standard; protein; 438
                                                                                                              92.5%;
93.8%;
                                                                                                                             al Similarity 93.8
394; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note=
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Napsin A; splicing; clone; screening; human liver cDNA library; aspartic protease; ss.

Human napsin A protein

WO9811236-A1

Homo

19-MAR-1998

Thu

sapiens WO9822597-A2

Homo

20-NOV-1997;

28-MAY-1998

20-NOV-1996; 09-MAY-1997;

Keolsch

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immunosuppressive; cytostatic; antiasthmatic; antiinflammatory; cancer; antiarteriosclerotic; antithyroid; antiasthmatic; antiinflammatory; cancer; antiateriosclerotic; antithyroid; antiathritic; antionforcective; antidabetic; anti-HVV; osteopathic; antiarthritic; treatment; cretinism; endocrinological; hypognadism; Sheehan syndrome; diabetes insipidus; hypothyroidism; adenocarcinoma; leukaemia; immunological; amyloidosis; acquired immune deficiency syndrome; AIDS; Addison's disease; arthritis; osteoporosis; atherosclerosis; infection; respiratory; allergy; asthma; emphysema; gene therapy; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New human aspartic protease polypeptide useful for treating and detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "Potential active site Asp residue characteristic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 active site Asp residue characteristic
                                                                                                                                                                                                                                                                                                                                                                                                                                                note= "Potential Tyrosine kinase phosphorylation site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note= "Potential protein kinase C phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note= "Potential protein kinase C phosphorylation
                                                                                                                                                                                                                                                                                                                                                             mouse aspartic protease-like
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                                                                                                                                                                                                                                                                                                                                                                                                                'note= "Potential casein kinase phosphorylation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "Potential N-glycosylation site"
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                                                                                                                                                                                                                                                                        1. .21
/label= Signal peptide
/note= "Potential"
                                                                                                                                                                                                                                                                                                                           22. .433
/label= Mature_NHAP-2
/note= "Homologous to protein (GI 1906810)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aspartic proteases"
                                                                                                                                                                                                                                                      cocation/Qualifiers
              Aspartic Protease-2 (NHAP-2)
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                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents the human napsin A protein. The cDNA sequence that produces this protein was obtained by splicing together isolated napsin cDNA clones, which had been found by screening a human liver cDNA library. Napsin A is an aspartic protease which was isolated from human liver, however it has also been found to be present in other
                                                                                                                                                                                                                                                                                                                         New isolated aspartic protease, napsin, from human liver - potentially useful for, e.g. diagnosis and treatment of disease.
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84.8%; Score 1897; DB 2;
Best Local Similarity 86.0%; Pred. No. 1.4e-170;
Matches 361; Conservative 16; Mismatches 43;
                                                                                                                                                                                                     (OKLA-) OKLAHOMA MEDICAL RES FOUND.
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                                                                                                                  97WO-US021684
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97US-0046126P
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N-PSDB; AAV27036.
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18-MAY-2000

AAY44810;

AAY44810 ID AAY4 XX AC AAY4 XX DT 18-h

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The present sequence is human aspartic protease-2 (NHAP-2) encoded by CDNA obtained from human leucocyte cDNA library. NHAP-2 gene is located on chromosome 19413. NHAP has immunosuppressive, antiallergic, or chromosome 19413. NHAP has immunosuppressive, antiallergic, cytostatic, antiatrathriftammatory, antiatrateriosclerotic, antithyroid, antibacterial, neuroprotective, antidiabetic, anti-HIV, csteopathic and antiarthrifta cactivity. It is useful for treating and preventing endocrinological disorders like hypogonadism, Sheehan syndrome, diabetes insipidus, cretinism and hypothyroidism, cancers like adenocarcinona and leukaemia, immunojaical disorders like acquired immune deficiency syndrome (AlDS), Addison's disease, amyloidosis, arthritis, osteoporosis, atherosclerosis and microbial infections and respiratory disorders like allergy, asthma and emphysema. NHAP polynucleotides can be used in gene therapy and for diagnosis of disorders associated with expression of NHAP
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endocrinological disorders e.g. hypogonadism, Sheehan syndrome and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 433;
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84.3%; Score 1887; DB 3;
Best Local Similarity 85.7%; Pred. No. 1.2e-169;
Matches 360; Conservative 16; Mismatches 44;
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                                                                                                         1; Fig 2; 83pp; English.
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                                         diabetes insipidus.
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                                                                                                             Claim
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that encode them and antibodies raised against them. The proteins, antibodies and nucleic acids are useful in the diagnosis, prognosis, prevention and/or treatment or diseases and/or disorders involving vasoconstriction, gastrointestinal disorders, cardiovascular disorders (e.g. hypertension, erectile dysfunction, high blood pressure, coronary carchexia, disorders of small intestine, disorders of reproductive system (e.g. male infertility and/or impotence), testicular cancer, lung tumours and other hyperproliferative disorders, disorders of pulmonary system, central nervous system disorders, bone disorders, neurodegenerative diseases and behavioural disorders (e.g. Alzheimer's disease, Parkinson's disease, Huntington's disease, schizophrenia, mania, dementia, paranoia,
                                                                                                                                                                                                                                   inflammatory bowel disease; sepsis; acne; psoriasis; lupus erythematosus; neural system disorder; respiratory disorder; olfactory disorder; wound healing; chromosome X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to novel human proteins (NHP) and the nucleic acids
gastrointestinal disorder; cardiovascular disorder; hypertension; coronary heart disease; arteriosclerosis; anovaxia; obesity; bulimia; cachexia; male infertility; importence; testicular cancer; lung tumour; hyperproliferative disorder; pulmonary system disorder; pulmonary system disorder; pulmonary system disorder; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; Huntington's disease; Alzheimer's disease; Parkinson's disease; Huntington's disease; schizophrenia; mania; dementia; paranoia; panc disorder; learning disability; amyotropic lateral sclerosis; psychosis; autism; sleep disorder; immune system disorder; multiple sclerosis; ischaemic brain injury; stroke; infectious disease; diabetes mellitus; immunological disorder; asthma; AlDS; immunogen; acquired immunodeficient syndrome; leukaemia; hebumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   eventing and/or cardiovascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Endress GA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New human proteins, useful for diagnosing, treating, preventing prognosing disorders related to the proteins, including cardiova disorders, autoimmune disorders and reproductive disorders.
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19. .65
| label | Immunogenic_epitope
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/label= Immunogenic_epitope
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/label= Immunogenic_epitope
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                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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2000US-0236384P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-APR-2001; 2001WO-US010542.
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/label= ]
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Li Y, Dillon PJ;
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29-SEP-2000;
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IPKLPAVSFILGGVWFNLTAHDYVIQTTRNGVRLCLSGFQALDVPPPAGPFWILGDVFLG 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPKLPAVSFLLGGVWFNLTAHDYVIQTTRNGVRLCLSGFQALDVPPPAGPFWILGDVFLG 379
                                                                                                                                                                                                                                                                            88
          psychoses, autism, sleep disorders), immune system disorders (e.g., Hashimoto's thyroiditis), renal and musculo-skeletal system disorders, central nervous system disorders (e.g. multiple sclerosis, isohesmic brain injury and/or stroke), infectious diseases, diabetes mellitus, immunological disorders (e.g. asthma, acquired immunodeficient syndrome (AIDS), leukaemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, psoriasis and luque erythematosus), neural system disorders, reepiratory disorders, olfactory disorders and wound healing. The present sequence represents an NHP of the invention
                                                                                                                                                                                                                                                                                                                                                                                    112 YGTGRVHGILSEDKLIIGGIKGASVIFGELSGTQPGL--RFCPFDGILGLGFPILSVEGV
                                                                                                                                                                                                                                                                                                                                                                                                                                          RPPMDVLVEQGILDKPVFSFYLNRDPEEPDGGELVLGGSDPAHYIPPLTFVEVTVPAYWQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 EIGLGTPPQNFTVAFDTGSSNLWVPSRRCHFFSVPCWLHHRFDPKASSSFQANGTKFAIQ
                                                                                                                                                                                                                                                                                                                                    ---WLHHRFDPKASTP-SSQWDQFAIQ
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                                                                                                                                                                                                                                                                                                                                                                                                                        RPPMDVIJVEQGILDKPVFSFYLNRDPEEPDGGELVLGGSDPAHYIPPLTFVPVTVPAYWQ
                                                                                                                                                                                                                                                 PSGATLIRIPLHRVQPGRRTLNILRGWREPAELPKLGAPSPGDKPIFVPLSNYRDVQYFG
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                                                                                                                                                                                                                    Gaps
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disorder, learning disabilities, amyotropic lateral sclerosis,
                                                                                                                                                                                                                    45;
                                                                                                                                                                                         Length 390;
                                                                                                                                                                                       Score 1702.5; DB 4; Length
Pred. No. 3e-152;
7; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYVAVEDRGDMKSSARVGLARARTRGADLGWGETAQAQFPG 420
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                                                                                                                                                                                          76.1%;
83.3%;
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                                                                                                                                                               Sequence 390 AA;
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Matches
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LLAGEYIILCSEIPKLPAVSFLLGGVWFNLTAHDYVIQTTRNG-VRLCLSGFQALDVPPP 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FVPVTVPAXWQIHMERVKVGPRADSLCQGCAAILDIGTYLVITGPTEBIRALHAAIGGIP 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LGFPILSVEGVRPPMDVLVEQGLLDKPVFSFYLNRDPEEPDGGELVIGGSDPAHYIPPLT 248
                                                                                                                                                                                                                                                                                                                                                                                          invention describes novel human aspartic proteases and also ESTS from human cDNA libraries having partial DNA sequences which encodes an aspartic protease. Compounds which inhibit aspartic protease, especially antibodies can be used in therapy where needed. The protease can also be used in therapy where needed. The protease can also be are the processing of endothelin and pro-opiomelanocortin prohormones. They may also be involved in the processing of serum amyloid A protein
                                                                                                                                                                                                                                                                                                                                                                                   The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSLLLLPLLINVEPAGATLIRIPLRQVHPGRRTINLLRGWGKPAELPKLGAPSPGDKPASV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLSNYRDVQYFGEIGLGTPPQNFTVAFDTGSSNLWVPSRRCHFFSVPCWLHHRFDPKASS
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                                                                                                                                                                                                                                                                                                          Human ampartic protease and related DNA - which may be involved processing of endothelin and pro-opiomelanocortin pro-hormone(s)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75.0%; Score 1678.5; DB 2; Length 449; 81.1%; Pred. No. 6.8e-150; ive 18; Mismatches 55; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                 present sequence represents a human aspartic protease.
'note= "encoded by GNC"
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                                                                                                                                                                                                                                                                                                                                                        Clain 14; Page 23; 32pp; English
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                                                                                                                                          97WO-GB002426
                                                                                                                                                                    96GB-00018966
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N-PSJB; AAV28624.
                440
                                         Misc-difference 442
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             Misc-difference
                                                                                                                                           09-SEP-1997;
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                                                                                   W098:L1236-A1
                                                                                                               19-MAR-1998
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367 AGPFWILGDVFLGTYVAVFDRGDMKSSARVGLARARTRGADLG 409

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RESULT 13 AAY79177

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Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase; ligase; hyperproliferative disorder; immunodeficiency disorder; autoimmune disorder; neurological disorder; metabolic disorder; inflammatory disorder; cardiovascular disorder; reproductive disorder; blood-related disorder; infectious disorder; cytostatic; anti arthritic; nephrotropic; anticoagulant.
                                                                                                 PPPAGPFWILGDVFLGTYVAVFDRGDMKSSARVGLARARTRGADLGWGBTAQAQF----P
                                                                                                                                                                                  244 IPPLTFVPVTVPAYWQIHMERVKVGPGLTLCAKGCAAILDTGTSLITGPTEEIRALHAAI
                    GGIPLLAGEYIILCSEIPKLPAVSFLLGGVWFNLTAHDYVIQTTRNGVRLCLSGFQALDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human enzyme polypeptide #152.
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11.-JUL-2000; 2000US-0217496P.

14.-JUL-2000; 2000US-021829P.

26.-JUL-2000; 2000US-0220964P.

14.-AUG-2000; 2000US-0224519P.

14.-AUG-2000; 2000US-0224519P.

14.-AUG-2000; 2000US-022514P.

14.-AUG-2000; 2000US-0225214P.

14.-AUG-2000; 2000US-0225214P.

14.-AUG-2000; 2000US-0225264P.

14.-AUG-2000; 2000US-0225266P.
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02-MRR-2000; 2000US-0186550P.

16-MRR-2000; 2000US-0189874P.

17-MRR-2000; 2000US-0190076P.

19-MRY-2000; 2000US-0194123P.

19-MRY-2000; 2000US-0205515F.

07-UNN-2000; 2000US-0205515F.

28-UNN-2000; 2000US-0205915P.
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2000US-0216647P.
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18-AUG-2000; 2000US-0226279P
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07-JUL-2000;
07-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is that of a mouse haematopoietic stem cell (HSC) specific protein. It is an example of claimed HSC-specific proteins (see AAY29176-93) predicted from novel isolated HSC-specific proteins (see AAY29176-93) predicted from novel isolated HSC-specific nucleic acids (see AAX294077-131). The HSCs are especially primitive HSCs (PHSCs) such as umbilical cord cells, bone marrow cells and foetal liver cells. The encoded proteins are growth factors, transcription factors splicing factors, transport proteins, translation factors or replication factors that modulate HSC activity, especially differentiation or replication. The invention provides claimed methods: of or identifying PHSC-specific nucleic acids, for generating a stem cell/progenitor cell from PHSCs; for identifying the presence in a sample of a compound that modulates HSC activity; for using such a compound to treat an immune system condition, especially leukaemia; for introducing exogenous nucleic acid into a HSC; and for ex vivo expansion of HSCs. Also claimed are coverors, host cells, and an antibody that specifically binds a an HSC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 NPSFVPLSKFMNTQYFGTIGLGTPPQNFTVVFDTGSSNLWVPSTRCHFFSLACWFHHRFN 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 KPIFVPLSNYRDVQYFGEIGLGTPPQNFTVAFDTGSSNLWVPSRRCHFFSVPCWLHHRFD 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 LQPLLLLLPLL---NVEPSGATLIRIPLHRVQPGRRTLNLLRGWREPAELPKLGAPSPGD 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MSPLILLLLLCLLGNLEPEEAKLIRVPLORIHLGHRILNPLNGWEQLAELSR--TSTSGG 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PKASSSFQANGTKFAIQYGTGRVDGILSEDKLTIGGIKGASVIFGEALWEPSLVFAFAHF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hematopoietic stem cell signaling proteins modulating replication and differentiation for treating immune system disorders and leukemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 3; Length 419;
                                                                                                                                                               stem cell; immune system disorder; leukaemia; immunomodulator; therapy; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Pred. No. 9e-139;
37; Mismatches 79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69.7%; Score 1560.5; 70.3%; Pred. No. 9e-1
                                                                                                                          Haematopoietic stem cell specific protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 21; Page 214-16; 256pp; English.
          AAY79177 standard; protein; 419 AA.
                                                                                                                                                                                                                                                                                                                                                                                  98US-00138132.
                                                                                                                                                                                                                                                                                                                                           99WO-US019052
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Best Local Similarity 70.3*
Matches 296; Conservative
                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                          (UYPR-) UNIV PRINCETON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Moore K;
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                                                                                                                                                                   stem
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                                                                                                                                                                                                                                                                WO200011168-A2.
                                                                                                                                                               Haematopoietic
antileukaemic;
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                                                                                                                                                                                                                           Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                  21-AUG-1998;
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2000US-0227182P.
2000US-0229287P.
2000US-0229343P.
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2000US-0229343P.
2000US-022943P.
2000US-022943P.
2000US-022943P.
2000US-0231243P.
2000US-0231968P.
2000US-0232940P.
2000US-023298P.
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2000US-0236369P.
2000US-0236370P.
2000US-0237037P.
2000US-0237038P.
2000US-0237038P.
2000US-0237038P.
2000US-0237038P.
2000US-0237038P.
2000US-0239935P.
2000US-0239935P.
2000US-0239937P.
2000US-0239937P.
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2000US-0241787P
2000US-0241808P
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2000US-0244617P
2000US-0246476P
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2000US-0246613P
       22-AUG-2000;
22-AUG-2000;
30-AUG-2000;
30-AUG-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
05-SEP-2000;
05-SEP-2000;
06-SEP-2000;
06-SEP-2000;
                                                                                                               08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
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29-SEP-2000;
29-SEP-2000;
02-OCT-2000;
02-OCT-2000;
02-OCT-2000;
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08-NOV-2000;
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17-NOV-2000; 2000US-0249208F.
17-NOV-2000; 2000US-0249210F.
17-NOV-2000; 2000US-0249211F.
17-NOV-2000; 2000US-0249211F.
17-NOV-2000; 2000US-0249211F.
17-NOV-2000; 2000US-0249211F.
17-NOV-2000; 2000US-0249211F.
17-NOV-2000; 2000US-0249217F.
17-NOV-2000; 2000US-0249217F.
17-NOV-2000; 2000US-0249217F.
17-NOV-2000; 2000US-0249217F.
17-NOV-2000; 2000US-024924F.
17-NOV-2000; 2000US-024924F.
17-NOV-2000; 2000US-024924F.
17-NOV-2000; 2000US-024926F.
17-NOV-2000; 2000US-024926F.
17-NOV-2000; 2000US-024926F.
17-NOV-2000; 2000US-024929F.
17-NOV-2000; 2000US-0249300F.
01-DEC-2000; 2000US-0251030F.
05-DEC-2000; 2000US-0251030F.
05-DEC-2000; 2000US-0251030F.
06-DEC-2000; 2000US-025108F.
08-DEC-2000; 2000US-025108F.
08-DEC-2000; 2000US-025108F.
08-DEC-2000; 2000US-025108F.
08-DEC-2000; 2000US-025108F.
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Rosen CA, Barash SC, Ruben SM,

(HUMA-) HUMAN GENOME SCI INC

WPI; 2001-465566/50. N-PSDB; AAS40936.

Novel polypeptides and polynucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous diseases.

Claim 11; SEQ ID NO 1062; 1180pp; English

The present invention relates to the isolation of novel human enzyme polypeptides, and the CDNA (AAS40785, AAS41684) and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of a wide range of disorders including hyperproliferative disorders (e.g. cancer), immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g. arthritis), neurological disorders (e.g. AIDS) autoimmune disorders (e.g. arthritis), intilammatory disorders (e.g. asthma), cardiovascular disorders (e.g. atheroselerosis), blood-related disorders (e.g. lamenoution disorders (e.g. influence). The polymucleotides of the invention can also be used in gene therapy. AAU22915-AAU23814 represent the novel human enzyme polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at

Sequence 288 AA;

1; Indels 0; Gaps 60.0%; Score 1343; DB 4; Length 288; 99.6%; Pred. No. 2.1e-118; ive 0; Mismatches 1; Indels Query Match 60.0 Best Local Similarity 99.6 Matches 251; Conservative

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09 1 MSPPPLLQPLILLLPLINVEPSGATLIRIPLHRVQPGRRTINLLRGWREPAELPKLGAPS

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                        120
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  62
                                                                                                                                                                                                                                                                                                                                        Secreted protein; immunosuppressive; antiarthritic; antirheumatic; antipoliferative; Cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; human; opthalmalogical; gene therapy.
                       PGDKPIFVPLSNYRDVQYFGEIGLGTPPQNFTVAFDTGSSNLWVPSRRCHFFSVPCWLHH
                                       63 PGDKPIFVPLSNYRDVQYFGEIGLGTGTPPQNFTVAFDTGSSNLWVPSRRCHFFSVPCWLHH
                                                                                                                                  AHFDGILGLGFPILSVEGVRPPMDVLVEQGLLDKPVFSPYLNRDPEEPDGGELVLGGSDP
MSPPPLLQPLLLLDPLLNVEPSGATLIRIPLHRVQPGRRILNLLRGWREPAELPKLGAPS
                                                                    RFDPKASSSFQANGTKFAIQYGTGRVDGILSEDKLTIGGIKGASVIFGEALWEPSLVFAF
                                                                                          123 RFDPKASSSFQANGTKFAIQYGTGRVDGILSEDKLTIGGIKGASVIFGEALWEPSLVFAF
                                                                                                                  AHFDGILGLGFPILSVEGVRPPMDVLVEQGLLDKPVFSFYLNRDPEEPDGGELVLGGSDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Soppet DR;
Shi Y, Choi GH;
                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Xaa can be any amino acid"
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Duan DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Komatsoulis GA, Baker KP, Bir
Moore PA, Wei P, Ebner R, Di
, Ni J, Ruben SM, Barash SC;
                                                                                                                                                                                                                                                                                                                  Human secreted protein (clone Id HCRME12)
                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                               AAB85539 standard; protein; 262 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-JAN-2001; 2001WO-US001431.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-JAN-2000; 2000US-0179065P.
04-FEB-2000; 2000US-0180628P.
12-SEP-2000; 2000US-0231968P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC.
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HS, Moore PA, Wei
                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                               AHYIPPLIFVPV 252
                                                                                                                                                                                 AHYIPPLTFVPV 254
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N-PSDB; AAH46949.
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The invention provides novel human secreted proteins and polynucleotides encoding them. The secreted proteins can be expressed by standard recombinant methodology. The secreted proteins and polynucleotides are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They can also be used in diagnosing a pathological condition. The antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbent assays (ELISA). Disorders which are diagnosed or

17 isolated nucleic acid molecules encoding human secreted proteins, used to preventing, treating or ameliorating a medical condition.

Claim 11; Page 455-456; 482pp; English.

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hyperproliferative disorders e.g. neoplasms of the breast or liver, aradioascular disorders e.g. neoplasms of the breast or liver, earlionscular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and cordiar disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and pithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. The present sequence represents a human secreted protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 PGDKPIFVPLSNYRDVQYFGEIGLGTPPQNFTVAFDTGSSNLMVPSRRCHFFSVPCWLHH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 RFDPKASSSFQANGTKFAIQYGTGRVDGILSEDKLTIGGIKGASVIFGEALWEPSLVFAF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 PGDKPIFVPLSNYRDVQYFGEIGLGTPPQNFTVAFDTGSSNLWVPSRRCHFFSVPCWLHH 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MSPPPLLQPLLLLLPLLNVEPSGATLIRIPLHRVQPGRRTLNLLRGWREPABLPKLGAPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 AHFDGILGLGFPILSVEGVRPPMDVLVEQGLLDKFVFSFYLNRDPEEPDGGELVLGGSDP
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                                                                                                                                                                                                                                                                                                                                              Length 262;
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                                                                                                                                                                                                                                                                                                                                         59.3%; Score 1328; DB 4; 97.6%; Pred. No. 4.8e-117; ive 0; Mismatches 6;
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Matches 249; Conservative
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time: 103.065 secs
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                                                                                                                              June 2, 2004, 20:07:29; Search time 14.9222 Seconds (without alignments) 1966.411 Million cell updates/sec
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459
1 MKLVTIFYLVTISLCSYSAT......LGPEASEAVKKLLEALSHIV
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                               1017041 seqs, 315518202 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                    OM protein - protein search, using sw model
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1: Sp_archea:*
2: Sp_bacteria:*
3: Sp_fungi:*
4: Sp_human:*
5: Sp_invertebrate:*
6: Sp_nammal:*
7: Sp_nfo:*
7: Sp_plage:*
8: Sp_organie:*
1: Sp_plage:*
1: Sp_plage:*
1: Sp_virus:*
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Q32836
Q32836
Q9W725
Q9W7254
Q7X254
Q91AR8
Q8WY6
Q800U1
Q8WZP4
Q8WZP4
Q7WD5
Q9LVP3
Q9LVP3
Q8XMB4
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length DB
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Sequence:
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ALIGNMENTS

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1426 MKRYDSIQKLINETSHL 1442
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                                                                                                                                                                             Query Match
Best Local Similarity
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GO; GO: 0005524; F.ATP binding; IEA.
GO; GO: 0004009; F.ATP-binding cassette (ABC) transporter acti. . .; IEA.
GO; GO: 000166; F:nucleotide binding; IEA.
GO; GO: 0006810; P:transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chen J., Jacques C., Cutler C., Mercier B., Boeuf G., Ferec C.; "Salmo salar cystic fibrosis transmembrane conductance regulator I."; Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
                                                                                                                  Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
Geraniales; Geraniaceae; Pelargonium.
NCBI_TaxID=4031;
                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=94363755; PubMed=8082181;
Downlie S.R., Katz-Downle D.S., Wolfe K.H., Calie P.J., Palmer J.D.;
Internal Structure and evolution of the largest chloroplast gene (ORF2280):
internal plasticity and multiple gene loss during angiosperm
evolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salmo salar (Atlantic salmon).

Bukaryota: Metazota; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii, Neopterygii; Teleostei; Buteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     33;
                                                                                                                                                                                                                                                                                                                                                                                                                           DB 8; Length 2109;
                                                                                                                                                                                                                                                       CURT. Genet. 25:367-378(1994).

REMBL; M83200; AAA73173.1; -.

PIR; T31352; T31352.

GO; GO:0005507; C:chloroplast; IEA.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:000166; F:ATP binding; IEA.

RO; GO:000166; F:ATP binding; IEA.

RIHCEPTO; IPRO08543; DUF825.

RIHCEPTO; IPRO08543; DUF825.

RANAT; SWO382; AAA; I.

ATP-binding; Chloroplast.

SEQUENCE 2109 AA; 245645 MW; 948980477223DE8C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Cystic fibrosis transmembrane conductance regulator I.
                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  24;
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                          PRT; 2109 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                         17.1%; Score 78.5; 24.0%; Pred. No. 31
                                                                                                Pelargonium hortorum (Common geranium)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003593; AAA ATPase
                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 24.09
                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                             Chloroplast.
                                                                                   ORF2280.
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Q98TY5;
                                    232836;
                        032836
RESULT 2
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              032836
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RP NELLINB=21396404; PubMed=11504857; RX 121

RX MELLINB=21396404; PubMed=11504857; RX Cutler C., Jacques C., Boeuf G., Denamur E., Lecointre G., Macrine J.M., Cutler C., Jacques C., Boeuf G., Denamur E., Lecointre G., RA Chen J.M., Cutler C., Jacques C.; Boeuf G., Denamur E., Lecointre G., Marcier J.M., Cutler C., Jacques C.; Boeuf G., Denamur E., Lecointre G., Marcier J.M., Mall Ballolle Conductance RT Revulator: Implications for Structure and Disease Models.";

R EQUIAGRAIN BELONGS TO THE ABC TRANSPORTER FAMILY.

C. - SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.

CR EMEL, API55237; AAD38404.1; - AD38404.1; - AD38404.1; - AD38404.1; - BAC GO:00016021; C.; Litegral to membrane; IEA.

GO; GO:00016021; C.; Litegral to membrane; IEA.

GO; GO:000610; F:ATP-binding cassette (ABC) transporter acti. . .; IEA.

GO; GO:000610; F:ATP-binding cassette (ABC) transporter acti. . .; IEA.

GO; GO:000610; F:ATP-binding cassette (ABC) transporter.

InterPro; IPR001359; AAA_ATPase.

DR InterPro; IPR001359; AAA_ATPase.

DR InterPro; IPR001359; AAA_Ciransporter.

INTERPAS; TIGR00185; ABC_transporter; 2.

R FEGM; PR000064; ABC_transporter; 2.

R TIGRRAMS; TIGR01271; CFTR protein; 1.

PROSITE; PS00211; ABC_TRANSPORTER 1; 1.

DR PROSITE; PS00211; ABC_TRANSPORTER 1; 1.

R TIGRRAMS; TIGR01271; CFTR protein; 1.

R PROSITE; PS00211; ABC_TRANSPORTER 1; 1.

R PROSITE; PS00211; ABC_TRANSPORTER 1; 1.
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Salmo salar (Atlantic salmon).
Stalmo salar (Atlantic salmon).
Stalmo salar (Atlantic salmon).
Stalmopterygii; Neopterygii; Teleostei; Buteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
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R InterPro; IPR001140; ABC_TW_transpt.
R InterPro; IPR003439; ABC_transporter.
InterPro; IPR003439; ABC_transporter.
InterPro; IPR00545, ABC_transporter.
R Pfam; PF00664; ABC_membrane; 2.
R Pfam; PF000606; ABC_tran; 2.
R Probom; P0000006; ABC_transporter; 1.
R SMART; SM00380; AAA; 301202; 1.
R TIGRFAMS; TIGR01271; CFTR_protein; 1.
R PR05ITB; PS00211; ABC_TRANSPORTER, 1; 1.
R PR05ITB; PS0031; ABC_TRANSPORTER, 2; 2.
ATP-binding; Transmembrane; Transport.
SEQUENCE 1430 AA; 167815 MW; 1A65781EABC79FB5 CRC64;
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SEQUENCE 1519 AA; 171239 MW, F4A67DF22898240C CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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16.7%; Score 76.5; D)
1 Similarity 36.4%; Pred. No. 36;
28; Conservative 10; Mismatches
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1 Similarity 36.4%; Pred. No. 35;
28; Conservative 10; Mismatches
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Local Similarity
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RY Adjuster FROM N.A.

REDLINE=98191134; PubMed=9530103;

RA divergent CFTR homologue: highly regulated salt transport in the adjuster T.D., Tucker S.J., Marshall W.S., Higgins C.F.;

RT Adjuster CFTR homologue: highly regulated salt transport in the euryhaline teleost F. heterociitus, ';

R. divergent CFTR homologue: highly regulated salt transport in the men post of colonology in the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the salt of the sa
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterrygii; Neopterrygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterrygii; Percomorpha; Atherinomorpha;
Cyprinodontiformes; Fundulidae; Fundulus.
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ive 14; Mismatches 21; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Cystic fibrosis transmembrane conductance regulator.
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Last sequence update)
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              VDKLAPLPLDNILPFMDP--LKLLLKTLG-----
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                                                                                                                                                                                                       ----EAVKKLLEALSHL
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les 27; Conserv
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ATP-binding; 7
SEQUENCE 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O7YZ54;
01-OCT-2003
01-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 5
073677
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AC 07
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REPUINE-21396404; PubMed=11504857;

RX MEDLINE-21396404; PubMed=11504857;

RA Chen JM., Cuttler C., Jacques C., Boeuf G., Denamur E., Lecointre G.,

RA Chen JM., Cattler C., Jacques C.,

RA Chen JM., Cattler C.,

RY Regilator: Implications for Structure and Disease Models.";

RO I Biol. Evol. 18:1771-1788 (2001).

C. -- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.

DR EMB., AF161070; AARTA 19:171-1788 (2001).

CO CO:0016021; C:integral to membrane; IEA.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:00016021; C:integral to membrane; IEA.

GO; GO:00016021; C:integral to membrane; IEA.

GO; GO:0001604; F:ATP binding; IEA.

GO; GO:000166; F:nucleotide binding; IEA.

GO; GO:00016810; P:transport; IEA.

GO; GO:0001401; ABC_TMITANETER:

InterPro; IPR003439; ABA ATPRASE.

InterPro; IPR003439; ABC_TMITANETER:

InterPro; IPR003439; ABC_TMINETER:

InterPro; IPR00005; ABC_TMINETER:

Pfam; PR00664; ABC membrane; 2.

PFam; PR006065; ABC_TMINETER:

PR PRODOM: PD000006; ABC_TMINETER:

PR PRODOM: PD000006; ABC_TMINETER:

PRODOM: PD000006; ABC_TMINETER:

PRODOM: PD000006; ABC_TMINETER:

PRODOM: PD0000006; ABC_TMINETER:

PRODOM: PD000006; ABC_TMINETER:

PRODOM: PD0000006; ABC_TMINETER:

PRODO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bankier A.T., Spriggs H.F., Fartmann B., Konfortov B.A., Madera M., Vogel C., Teichmann S.A., Ivens A., Dear P.H.;
"Integrated mapping, chromosomal sequencing and sequence analysis of Gryptosporidium partum.";
Gryptosporidium partum.";
Gerome Res. 0:0-0(2003).
EMEL; BX538353; CAD98273.1; -.
SEÇUENCE 481 AA; 54314 MW; D7BEAB422FA18886 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
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TIGREAMS; TIGR01271; CFTR protein; 1.
PROSITE; PSO0211, ABC TRANSPORTER 1; 1.
PROSITE; PSS00931; ABC TRANSPORTER 2; 2.
ATP-binding; Transmembrane, Transport.
SEQUENCE 1518 AA; 171136 MW; B3579B15820BA7F4 CRC64;
                                                                                                                                                                                             Bukāryota, Alveolata, Apicomplexa, Coccidia, Bimeriida,
Crrptosporidiidae, Cryptosporidium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-077-2000 (TrEMBLrel. 15, Created)
01-077-2000 (TrEMBLrel. 15, Last sequence update)
01-077-2003 (TrEMBLrel. 25, Last amontation update)
Cystic fibrosis transmembrane conductance regulator II.
01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Glutamine synthetase, probable.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16.0%; Score 73.5; Dl
24.4%; Pred. No. 23;
:ive 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |::: |:::|
246 QSADIVESIRYLIKGIAH 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80 -----EAVKKLLEALSH 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19; Conservative
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                                                                                                                                              Cryptosporidium parvum.
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Q836X7;

EF0967

0836X7

RESULT 8

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Q836X7

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aerophilum.";

Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).

EMBL; AE009827; AAL63563.1; -..

GO; GO:0016020; C:membrane; IEA.

GO; GO:00016021; E:ATP binding; IEA.

GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti...; IEA.

GO; GO:0016491; F:ATP-binding cassette (ABC) transporter IEA.

InterPro; IPR003499; ABC transporter.

InterPro; IPR002869; POR.

InterPro; IPR00209014; Transketo_Clike.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Sodium channel 4 (Fragment).
Ictalurus punctatus (Channel catfish).
Ictalurus punctatus (Channel catfish).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes; Ictaluridae; Ictalurus.
                                                                                                                                                                              "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
                                                                                                           Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.6%; Score 71.5; DB 17; Length 542; 26.3%; Pred. No. 41; ive 22; Mismatches 33; Indels 1;
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Pred. No. 42;
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Lu Y., Liptreato G.F., Zakon H.H.;

Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AY20435, AA060423.1; -.

RGO: GO:0016020; C:membrane; IRA.

GO: GO:0005261; F:cation transport; IEA.

Interpro; IPR001682; Ca/Na_pore.

Interpro; IPR001682; Ca/Na_pore.

Interpro; IPR005821; Ion_trans.

Interpro; IPR005821; Interpro; IPR005820; Interpro; IPR005821; Interpro; IPR05821; Interpro; IPR05821; Interpro; IPR05821; Interpro; IPR05821; Interpro; IPR05820; IPR05820; INTERPO; IPR05820; IPR05820; IPR05820; IPR05820; IPR05820; IPR05820; IPR05820; IPR058
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 542 AA; 60066 MW; D2BC3472E6B70FDD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF01558; POR; 1.
Pfam; PF01855; POR_N; 1.
PRCSITE; PS00211; ABC_TRANSPORTER_1; 1.
SEQUENCE FROM N.A.
STRAIN=IM2 / ATCC 51768 / DSM 7523;
MEDLINE=21664397; PubMed=11792869;
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31.3%;
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Best Local Similarity 31.33
Matches 26; Conservative
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                                                                                                                                                                                                                                                                      1394 LSKARITLLDEPSAYLDPITLOVLRKTLKQSFSNCTVILSEHRVEPLLECQSFLMIEGSS 1453
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                                                                                                                                                                                              31 VDKLAPLPLDNILPFMDP--LKLLLKTLG-----ISVEHLVEGLRKCVNELGPEAS- 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIR=V583 / ATCC 700802;
STRAIR=V583 / ATCC 700802;
PAULINE=22550657; PubMed=12663927;
Paulsen I.T., Baneriei L., Myers G.S.A., Nelson K.E., Seshadri R., Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F., Tettelin H., Dodson R.T., Umayam L., Brinkac L., Banann M., Daugherty S., DeBoy R.T., Durkin S., Kolonay J., Madupu R., Nelson W., Vamathevan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H., Utterback T., Radune D., Ketchum K.A., Dougherty B.A., Fraser C.M.; Wole G. mobile DNA in the evolution of vancomycin-resistant Science 299:2071-2074(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
NCBI_TaxID=1351;
                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34; Indels 10;
                                                                                                                       15;
                                           Length 1518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 16; Length 630;
                                                                                                                   24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pyrobaculum aerophilum.
Archaea; Crenarchaecta; Thermoprotei; Thermoproteales;
Thermoproteaceae; Pyrobaculum.
NCBI_TaxID=13773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            630 AA; 72204 MW; 3DBFCDA67DF4FDAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57 GISVE---HLVEGLRKCVNELGPEASEAVKKLLEALSHL 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2002 (TrEMBLrel. 20, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) 2-oxoacid ferredoxin oxidoreductase alpha subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last annotation update)
                                           DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enterococcus faecalis (Streptococcus faecalis)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.9%; Score 73; DB 1
26.3%; Pred. No. 34;
rative 29; Mismatches
                                       Query Match
16.0%; Score 73.5; DB
Best Local Similarity 35.1%; Pred. No. 74;
Matches 27; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       630 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                             1454 MKRYDSIQKLLNETSHL 1470
                                                                                                                                                                                                                                                                                                                                                     80 ----EAVKKLLEALSHL 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR007621; DUF477.
Pfam; PF04536; DUF477; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE016950; AA08074.1;
TIGR; EF0967; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best_Local Similarity 26.33
Matches 26; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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SEQUENCE 630 AA
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01-OCT-2003
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71

Gaps

1;

2;

Gaps

16;

Pred. No. 42; 8; Mismatches 33; Indels

7 FLLVTISLCSYSATAFLINKVPLPVDKLAPLPLDNILPFMDPLKLLLKTLGISVEHLVEG 66

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Q8ZWY6

RESULT 9

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OBZWY6

RESULT 11 28W2P4

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407 LLISISIPDWCSYDGITF-----ETFRAAPRPFGNAVSYVNSAFLARSSLDAASGSHL 459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 LLVTISL---CSYSATAFLINKVPLPVDKLAPLPLDNILPFMDPLKLLLKTL-GISVEHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Supermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
Supermatophyta; Massicales; Brassicaceae; Arabidopsis.
               01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Pucative aldehye oxidase.
05JNAA0087H07.7.
05JNAA0087H07.7.
Sharyota; Viridiplantae cultivar-group).
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ekhrartoideae; Oryzeae; Oryza,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                  STRAIN=cv. Nipponbare;
The Rice Chromosome 10 Sequencing Consortium;
"In-depth view of structure, activity, and evolution of rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
15.3%; Score 70; DB 10; Length 106;
Best Local Similarity 27.3%; Pred. No. 11;
Matches 21; Conservative 16; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                             SEĞUENCE FROM N.A.
STRAIN-cv. Nipponbare;
Bue.l C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
Subnitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; ASTO7054; AAPS2052.1; -.
SEQUENCE 1358 AA; 145452 MW; 75B3A692C75D537D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clones.";
DNA Res. 7:131-135(2000).
EMBL; AD18121; BAB01992.1; -
SRQUENCE 106 AA; 11542 MW; 6AE232BFD4C5D0DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-071-2000 (TrEMBLrel. 15, Created)
01-071-2000 (TrEMBLrel. 15, Last sequence update)
01-071-2000 (TrEMBLrel. 15, Last annotation update)
Genomic DNA, chromosome 3, Pl clone: MXE2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 15.4%; Score 70.5; DB 10 1 Similarity 27.9%; Pred. No. 1.4e+02; 24; Conservative 13; Mismatches 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20277480; PubMed=10819329;
                                                                                                                                                                                                                                                                                                                                                     Science 300:1566-1569(2003)
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                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                         NCB. TaxID=39947;
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                                                                                                                                                                                                                                                                                                                                    chromosome 10
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                     358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kim H.-R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DE4-----
                                                                                                                                                                                                                                                                                                                                                        Oryza sativa (Rice).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gramene, OBW224; -..

R Gramene, OBW224; -..

R GO; GO:0005489; F:electron transporter activity; IEA.

R GO; GO:0016491; F:exidoreductese activity; IEA.

R GO; GO:0016472; F:eprotein kinase activity; IEA.

R GO; GO:00066118; F:eprotein kinase activity; IEA.

R GO; GO:0006618; P:protein kinase activity; IEA.

R GO; GO:0006618; P:protein mino acid phosphorylation; IEA.

R InterPro; IPR00288; 2Fe2S_Ed BS.

R InterPro; IPR00889; 2Fe2S_Ed BS.

R InterPro; IPR008107; Co_deh_flav.

R InterPro; IPR00214; Addxan dh hamm.

R InterPro; IPR00111; Ferredoxin.

R InterPro; IPR00119; Prot_kinase.

R Pfam; PF03138; Ald Xan dh C2; 1.

R Pfam; PF03138; Ald Xan dh C2; 1.

R Pfam; PF03138; Ald Xan dh C2; 1.

R Pfam; PF03131; Fazz_2; 1.

R Pfam; PF03111; Fezz_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen M.,
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wing R.A., Yu Y., Yang T.J., Nah G., Soderlund C., Chen Pambo T., Saski C., Henry D., Oates R., Simmons J.;
"Rice Genomic Sequence.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
-!- COPACTOR: BINDS 1 2FE-2S CLUSTER (BY SIMILARITY).
EMBL; AC099733; AAL70116.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1358 AA; 145453 MW; 75B3A692C75D537D CRC64;
                                                                                                                                                                                                                                                                         01-MAR-2002 (TrEMBLrel. 20, Last sequence update) 01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.4%; Score 70.5; DB 10; 27.9%; Pred. No. 1.4e+02; tive 13; Mismatches 38;
                                                                                                                                                                                                           1358 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF01799; fer2 2; 1. ProDom; PD186071; 2Fe-2S bind; 1. PROSTIE; PS00197; 2FE2S FEREDOXIN; 1. PROSITE; PS00107; PROTEIN_XINASE_ATP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 VEGLRKCVNELGPEASEAVKKLLEAL 89
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                                                                                                      359 MRVVVNALFGAIPSIVNVLLVCL 381
                                                                                                                                                                                                                                                     Created)
                                                             8
                                                                                                                                                                                                         PRT;
                                                               67 LRKCVNELGPEASEAVKKLLEAL
                                                                                                                                                                                                                                                     01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                Putative aldehyde oxidase.
OSJNAA0087H07.7.
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Matches 24; Conservative
                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gramene; Q8W2P4;
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                        315
                                                                                                                                                                                                           Q8W2P4
Q8W2P4;
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3,

Gaps

11;

Indels

38;

Length 1358;

63

5;

Gaps

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PRT; 1358 AA.

PRELIMINARY;

Q7XH05 RESULT 12 Q7XH05

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Search completed: June 2, 2004, 20:21:27
Job time : 17.9222 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 VYTVYPAVVKKFNDMELDYCCGGNKSLELALKEKGVDVDKFVEDLNKEFKEFKFENSQYV 73
                 1 MKFTTLTLLVLVTVIQLSPTLIRATMVEGPTGDVTCNPMDVIVPCLLPLTNSKILPTPHC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1] — SEQUENCE FROM N.A. FU G., Lin W., Gu W.Q., Zhu G.F., Tu Y.F., Fu G., Wang S.Y., Ren S.X., Lv G., Lin W., Gu W.Q., Zhu G.F., Tu Y.F., Jia J., Xin H.F., Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y., Shao Y., Sun Y., Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W., Sheng H.H., Gu J.L., Chen S.T., Ni L., Zhu F.H., Han B., Feng Q., Sheng Y.C., Li Y., Zhu J.J., Zhao Q., Hu X., Liu Y.L., Mu J., Yu Z.,
1 MKLVTIFLLVTISLCSYSATAFLINKVPLPVDKLAPLPLDNILPFMDPL---KLL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Gaps
                                                                                                                                                                                                                                                                                                                                                             STRAIN-13 / Type A;
MEDLINE-21664373; PubMed-11792842;
Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
"Complete genome sequence of Clostridium perfringens, an anaerobic flesh-eater.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryza sativa (Rice).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                        Clostridium perfringens.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.3%; Score 70; DB 16; Length 232; 32.0%; Pred. No. 25; tive 9; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF03794; HHE; 1.
Pfam; PF04405; ScdA N; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 232 AA; 27555 WW; 5C3F5BRIFBB9ABEI CRC64;
                                                                                                                                                                                             01-MAR-2002 (TrEMBLrel. 20, Created)
1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein CPE0775.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:996-1001 (2002).
EMBL; AP003188; BAB80441.1; -.
InterPro; IPR007500; DUF542/ScdA_N.
InterPro; IPR005544; HHE.
                                                                                                                                                                    232 AA
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                                                           53 LKTLGISVEHLVEGLRK 69
                                                                            : ::|: :||
61 CQVMFMMMQHITINIRK 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25, OSJNBD0022F23.17, protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83 ----KKLLEALSHLV 93
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DWREKSSEELISHIV 88
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                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                NCBI_TaxID=1502;
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                                                                                                                                    RESULT 14
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Chen L., Fan D.L., Weng Q.J., Zhang L., Lu Y.Q., Yu S.L., Liu X.H., Lu T.T., Zhang Y.J., Lu Y., Li C., Li T., Zhang Y., Hu H., Jia P.X., Zhang Y.M., Ying K., Zhou B., Chen Z.H., Hao P., Zhang L., Wu M., Zhang R.Q., Guan J.P., Hong G.F., Submitted (SEP-2011) to the EMBL/GenBank/DDBJ databases.

EMBL, A606447; CAE02880.1; -- EADFA4BED0C7E49A CRC64;
                                                                                                                                                                                                                                                                     28;
                                                                                                                                                                                                              15.3%; Score 70; DB 10; Length 603; 27.4%; Pred. No. 66;
                                                                                                                                                                                                                                                                   12; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             52 LLKTLGISVEHLVEGLRKCVNELGPEASEAVKKLL 86
                                                                                                                                                                                                                                                                   26; Conservative
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us-09-700-770-7.rsp

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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2, 2004, 20:05:19; Search time 3.6175 Seconds (without alignments) 1338.637 Million cell updates/sec June Run on:

US-09-700-770-7 459 1 MKLVTIFLLVTISLCSYSAT......LGPEASBAVKKLLEALSHLV 93 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seg length: 0 Maximum DB seg length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	[d	mus n	0920d7 mus musculu	homod	рошо	metha	P16602 cowpox viru					P11684 homo sapien	0	Q58717 methanococc	P35395 hypophthalm		095968 homo sapien			pyrobac	092ax9 listeria in		_	•	P78562 homo sapien	P70669 mus musculu	P56145 helicobacte		٠.		092357 schizosacch	P15558 pseudomonas	α
SUMMARIES	ID	UGR1 HUMAN	UGR1 MOUSE	UGR2 MOUSE	UGR2 HUMAN	LPPB_HUMAN	YF09_METJA	ATI COMPX	RPC_BPPH1	SYFB_HELPJ	PSC3_RAT	MURD_RICPR		NIFS_AZOCH	YD21_METJA	PRL_HYPMO	CN4A_RAT	LPPA_HUMAN	Y102_BACHD	DCDA_VIBCH	SAHH PYRAE	METE_LISIN	YQOA_CAEEL	ZDHJ_HUMAN	HEM1_SYNPX	PEX_HUMAN	PEX_MOUSE		Y55B_MYCPN		NDDD_ALCXX	CHS5_SCHPO	PAC2 PSES3	LEPA_BUCAI
	DB -	Ч	Н	-1	-	Н	Н	Н	Н	Н	Н	Н		Н	-1	-	-	Н	Н	Н	Н	Н	Н	Н	Н	Н	Н	н	Н	Н	Н	-	-	н
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089084 mus musculu				Q9z7k9 chlamydia p							P41234 mus musculu
CN4A MOUSE	CN4A HUMAN	SZ10 HUMAN	RP35 BACAA	RS2 CHLPN	Y755 METJA	LEU3 PICJA	IMDH_MYCLE	RRPO_LYCVA	APY SOLTU	YSSL SYNY3	ABC2_MOUSE
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844	886	98	239	277	342	363	529	2210	454	562	2434
13.6	13.6	13.5	13.5	13.5	13.5	13.5	13.5	13.5	13.4	13,4	13.4
62.5	62.5	62	62	62	62	62	62	62	61.5	61.5	61.5
3.4	3.5	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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EMBL; AF274961; AAL25710.1; -.
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107
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28--FBB-2003
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UGR2_MOUSE
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                MKLVTIFLLVTISLCSYSATAFLINKVPLPVDKLAPLPLDNILPFMDPLKLLLKTLGISV 60
                                                                                                                                                                                                                                                                           1 MKLVTIFLLVTISLCSYSATAFLINKVPLPVDKLAPLPLDNILPFMDPLKLLKTLGISV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "UGRP1, a uteroglobin/clara cell secretory protein-related protein, is a novel lung-erriched downstream target gene for the T/EBE/NKX2.1 homeodomain transcription factor.";
Mol. Endocrinol. 15:2021-2036 (2001).
-! SUBGUNIT: Homodimer.
-! SUBCELLUIAR LOCATION: Secreted.
-! ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia<u>;</u> Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isold=Q920H1-3; Sequence=VSP_006726;
TISSUE SPECIFICITY: Highly expressed in lung.
SIMILARITY: Belongs to the uteroglobin family, UGRP subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Niimi T., Keck-Waggoner C.L., Popescu N.C., Zhou Y., Levitt R.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Uteroglobin-related protein 1 precursor (Secretoglobin family 3A member 2).
                                                                                                                                                                                                                     ;
                                                                                                                                                                                        DB 1; Length 93;
                                                                                                                                               PROTEIN 1.
                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=Q920H1-2; Sequence=VSP_006727, VSP_006728;
                                                                                                                                                           FBD4BFAC2BF33718 CRC64;
                                                                                                                                             UTEROGLOBIN-RELATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Event=Alternative splicing; Named isoforms=3; Name=C_i
                                                                                                                                                                                        Score 459; DB 1;
Pred. No. 1e-39;
0; Mismatches (
                                                                                                                                                                                                                                                                                                       EHLVEGLRKCVNELGPEASEAVKKLLEALSHLV 93
                                                                                                                                                                                                                                                                                                                               EHLVEGLRKCVNELGPEASEAVKKLLEALSHLV 93
                                                                                                                                                                                                                                                                                                                                                                                                                     0920H1; 0920H2; 0920H3;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                           139 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORMS A; B AND C)
                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21539178; PubMed=11682631;
                                                      EMBL, AF313455; AAL26215.1; -. EMBL; BC024232; AAH24232.1; -. Genew; HGNC:18391; SCGB3A2. MIM; 606531; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF274959; AAL25708.1; -.
EMBL; AF274960; AAL25709.1; -.
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22 93
93 AA; 10161 MW;
                                                                                                                                                                                        100.0%;
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Best Local Similarity
Local Somilarity
Local 93; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCGB3A2 OR UGRP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
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                                                                                                                                                           SEQUENCE
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SIGNAL
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation her Businformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKLVSIFLLVTIGICGYSATALLINRLPV-VDKL-PVPLDDIIPSFDPLKMLLKTLGISV
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKLVTIFLLVTISLCSYSATAFLINKVPLPVDKLAPLPLDNILPFMDPLKLLLKTLGISV
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N P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           homeodomain transcription factor.";
Mol. Endocrinol. 15:2021-2036(2001).
-!- FUNCTION: Potential growth inhibitory cytokine.
-!- SUBCELLULAR LOCATION: Secreted (By similarity).
-!- SUMILARITY: Belongs to the uteroglobin family. UGRP subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21396515; PubMed=11481438; Krop 1.E., Sgroi D., Porter D.A., Lunetta K.L., LeVangie R., Seth J. Krap 1.E., Sgroi D., Porter D.A., Lunetta K.L., LeVangie R., Seth J. Raalin C.M., Rhei E., Bosenberg M., Schnitt S., Marke J.R., Pagon Selina D., Razumovic J., Polyak K.; Belina D., Razumovic J., Polyak K.; and M. A. Putative oytokina highly expressed in normal but not cancerous mammary epithelial cells ", Proc. Natl. Acad. Sci. U.S.A. 98:9796-9801(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=21539178; PubMed=11682631;
Niihi I., Keck-Waggoner C.L., Popescu N.C., Zhou Y., Levitt R.C.,
Kimura S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Uteroglobin-related protein 2 precursor (Cytokine HIN-1) (High normal-1) (Secretoglobin family 3A member 1).
                                                                                                                                                                                                                                                                                                                                                                                                     7
                                                                                                                                                                   VSVLFLPMICAYPRDSKKQTFAFIERVFEQSKL
                                                                                                                                                                                    HLV (in isoform B).
/FTId=VSP 006726.
VIIICSY -> EALSHLV (in isoform A)
                                                                                                                                                                                                                                                                                                                                                            Length 139;
                                                                                                                                                 UTEROGLOBIN-RELATED PROTEIN 1
                                                                                                                                                                                                                                                                                                                                                                                                     6; Indels
                                                                                                                                                                                                                                                                                                                8A2FB080B41E65E4 CRC64;
                                                                                                                                                                                                                                                   /FTId=VSP 006727.
Missing (in isoform A).
/FTId=VSP 006728.
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4.3e-26;
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                                                                                                                                                                                                                                                                                                                                                                                                   11; Mismatches
                                                                                                                                                                                                                                                                                                                                                            71.0%; Score 326; 77.9%; Pred. No. 4
MGD; MGI:2153470; Scgb3a2.
GO; GO:0005576; C:extracellular; IDA.
GO; GO:0005515; P:protein binding; IPI.
InterPro; IPR006038; Utercglobin supf.
Pfam; PF01099; Utercglobin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86
                                                                                                                              POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EHLVEGLRKCVNELGPEASEAVKKLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                  Pred.
                                                                                                                                                                                                                                                                                                                139 AA; 15431 MW;
                                                                                                        Signal, Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SCGB3A1 OR UGRP2 OR HIN1.
                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                              21
139
139
                                                                                                                                                                                                                                                                         139
                                                                                                                                                                                                                                  91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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S S R R R F F S

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1 20 POTENTIAL.
21 104 UTERGACABIN-RELATED PROTEIN 2.
19 19 R -> A (IN REF. 2).
10185 MW; 1083873C8FAE8015 CRC64;
GO:0005125; F:cytokine activity; NAS. GO:0030308; P:negative regulation of cell growth; NAS. GO:0042127; P:regulation of cell proliferation; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AJ224172; CAA11864.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last seq
28-FEB-2003 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9925 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genew; HGNC:18396; SCGB1D2
                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                      Cytokine; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                       LPPB HUMAN
                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                          095969;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Signal.
                                                                                          CHAIN
                                                                                                                                                                                   Best Loca
Matches
   888
   SETTES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                  -------LPLDNILPF 45
                                                                                                                                                                                                                                                             18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             homeodomain transcription factor.";
Mol. Endocrinol. 15:2021-2036(2001).
-!- FUNCTION: Potential growth inhibitory cytokine.
-!- SUBCELIALIAR LOCATION: Secreted.
-!- SUBCELIALIAR LOCATION: Ascreted.
-!- TISSUE SPECIFICITY: Highly expressed in breast tissues. Absent in breast cancer cell lines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Krop I.E., Sgroi D., Porter D.A., Lunetta K.L., LeVangie R., Seth P., Kaelin C.M., Rhei E., Bosenberg M., Schnitt S., Marks J.R., Pagon Z., Belina D., Razumovic J., Polyak K.; Hillyl, a putative cytokine highly expressed in normal but not cancerous mammary epithelial cells."; Proc. Natl. Acad. Sci. U.S.A. 98:9796-9801(2001).
                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "UGRP1, a uteroglobin/clara cell secretory protein-related protein, a novel lung-enriched downstream target gene for the T/EBP/NKX2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: Belongs to the uteroglobin family. UGRP subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q96QR1; Q96PL0;
28-FFB-2003 (Rel. 41, Created)
28-FFB-2003 (Rel. 41, Last sequence update)
28-FFB-2003 (Rel. 41, Last annotation update)
28-FFB-2003 (Rel. 41, Last annotation update)
normal-1) (Secretoglobin family 3A member 1).
SCGBAA1 OR UGRP2 OR HINI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=21539178; PubMed=11682631;
Niimi T., Keck-Waggoner C.L., Popescu N.C., Zhou Y., Levitt R.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                19;
                                                                                                                                                              Length 104;
                                                                                                        UTEROGLOBIN-RELATED PROTEIN 2.
D62F0E601FB57A6D CRC64;
                                                                                                                                                                                                                                                                                                                             90
                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                          46 MDPLKLLLKTLGISVEHLVEGLRKCVNELGPEASEAVKKLLEALS
                                                                                                                                                                                                                                    1 MKLVTIFLLVTISLCSYSATAFLINKVPL----PVDKLAP
                                                                                                                                                           35.4%; Score 162.5; DB 1;
40.0%; Pred. No. 1.1e-09;
tive 17; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                     104 AA.
or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genew; HGNC:18384; SCGB3A1,
MIM; 606500; --
GO; GO:0005576; C:extracellular; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21396515; PubMed=11481438;
                                                                                     21 POS
104 UTI
10591 MW; I
                                EMBL; AF313456; AAL26216.1; -. MGD; MGI:1915912; Scgb3al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AY040564; AAK82942.1; -. EMBL; AF313458; AAL26217.1; -.
                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Human)
                                                                                                                          104 AA;
                                                                                                                                                                             Best Local Similarity
Matches 42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                    Cytokine; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                     UGR2 HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kimura S.;
                                                                                                                          SEQUENCE
                                                                                                                                                            Query Match
                                                                                      GNAL
                                                                                                                                                                                                                                                                                                                                                                                                                  HUMAN
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                                                                                                        51
                                                                                                                                                         59
                                                                                                                                                      1 MKLAALLGLCVALSCS-SARAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKL
                                                                                                        1 MKLVTIFLLVTISLCSYSATAFLINKVPLPVDKLAPL------PLDNILPFMDPLKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MUSCLE. EXPRESSED AS WELL IN THYMUS, TRACHEA, KIDNEY, STEROID RESPONSIVE TISSUES (PROSTATE, TESTIS, UTERUS, BREAST AND OVARY), AND SALIVARY GLAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                    10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: Belongs to the uteroglobin family. Lipophilin
Match 34.6%; Score 159; DB 1; Length 104; Local Similarity 43.6%; Pred. No. 2.4e-09; e8 44; Conservative 9; Mismatches 38; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                28-FBB-2003 (Rel. 39, Last sequence update)
Lipophilin B precursor (Secretoglobin family 1D member 2).
SGGB102 OR LIPHB.
                                                                                                                                                                                                                                           92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIPOPHILIN B.
17BB555ED035D1AF CRC64;
                                                                                                                                                                                                          52 LLKTLGISVEHLVEGLRKCVNELGPEASEAVKKLLEALSHL
                                                                                                                                                                                                                                                                                                                                                                                               90 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 75.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO, GO:0005615; C:extracellular space;
GO, GO:0005615; C:extracellular subf.
InterPro; IPR000329; Uteroglobin_subf.
Pfan; PF01.099; Uteroglobin; 1.
PRINTS; PR00486; UTEROGLOBIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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Matches

à g ò RESULT 6

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30 PVDKLAPLPLDNIL---PFMDP--LKLLLKT-LGIS-----VEHLVEGLRKCVNELG--- 75
                                                                                                                                                                                                                                                 Funahashi S., Sato T., Shida H.; "Clonding the major protein "Clonding and characterization of the gene encoding the major protein of the A-type inclusion body of cowpox virus."; J. Gen. Virol. 69:35-47(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MISCELLANEOUS: A CHARACTERISTIC FEATURE OF ATI IS THE FORMATION LARGE MASSES WITH NO SURROUNDING MEMBRANES IN THE CYTOPLASM OF INFECTED CELLS.
                                                                                                            Viluses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                        Patel D.D., Pickup D.J.;
"Messenger RNAs of a strongly-expressed late gene of cowpox virus contain 5'-terminal poly(A) sequences.";
EMBO J. 6:3787-3794(1987).
-!. FUNCTION: MATURE VIRUSES ARE OCCLUDED INTO THE AII, AND IT HAS BEEN ASSUMED THAT SUCH BODIES PROTECT THE VIRUS DURING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 X APPROXIMATE TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              150329 MW; F7904C9E1DE8D012 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
            01-AUG-1990 (Rel. 15, Last sequence update) 01-NOV-1990 (Rel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        144 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 45; 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 68.5;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISSEMINATION FROM ANIMAL TO ANIMAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X06343; CAA29650.1; -.
PIR; JQ0006; WWYZA.
Intervo: IPR007596; Pox A type inc.
Intervo: IPR04508; Pox_A type_inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-109 FROM N.A.
MEDLINE=88111568; PubMed=2828037;
                                                                                                                                                                                                             STRAIN=CPRO6;
MEDLINE=88089536; PubMed=2826668;
                                                 A-type inclusion protein (ATI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.9%;
36.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; D00319; BAA00222.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76 ---PEASEAVKKLLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    424 EYKTELEEAKRKLTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1284 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
es 27; Conserv
                                                                                         Cowpox virus (CPV)
                                                                                                                                                                                           SECUENCE FROM N.A.
                                                                                                                                                   NCBI_TaxID=10243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  666
690
721
752
781
812
843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Late protein;
DOMAIN
                                                                                                                                Orthopoxvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RPC_BPPH1
ID RPC_BPPH1
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REPEAT
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
              엄
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                                                                      1 MKLVTIFLLVTISLCSYSATAFLINKVPLPVDKLAPLPLDNILPFM---DPL-KLLLKTL 56
                                                                                                            ----EPCPALVSELLDFFPISEPLFKLSLAKF 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAINEJEL / DSW 2661 / ATCC 43067;
STRAINEJEL / DSW 2661 / ATCC 43067;
BULT C.J., White O., Olsen G.U., Zhou L., Fleischmann R.D.,
Butt C.J., White O., Olsen G.U., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Kerlawage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Raich C.I.,
Overbeek R., Kirkmess E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klank H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 FLINKVPLPVDKLAPLPLDNILPFMDPLKLLLKTLGISVEHLVEGLRKCVNELGPEASEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22; Indels
                               34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U67592; AAB99534.1; -.
PIR; D64488; D64488.
TIGR; MJ1509; -.
Hypothetical protein; Complete proteome.
SEQUENCE 153 AA; 17718 MW; OBLAABEDC831685B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Archaea; Euryarchaeota; Methanococci; Methanococcales; Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                   90
                                                                                                                                                     57 GISVEHLVE--GLRKCVNELGPE----ASEAVKKLLEALS
                                                                                                                                                                                      50 DAPPEAVAAKLGVKRCTDQMSLQKRSLIAEVLVKILKKCS
                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
              Pred. No. 0.57; ; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1284 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17; Mismatches
                                                                                                            1 MKLSVCLLLVTLALCCYQANA----
ATI_COWPX STANDARD;
P16602;
01-AUG-1990 (Rel. 15, Created)
                                                                                                                                                                                                                                                                                                                             (Rel. 40, Created)
(Rel. 40, Last seqn
(Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein MJ1509.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19; Conservative
                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               Methanococcus jannaschii.
                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ||:|:
145 AKKVLD 150
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              Similarity
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                                                                                                                                                                                                                                                                                                                                16-OCT-2001
16-OCT-2001
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                                                                                                                                                                                                                                                                                        YF09 METJA
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              Best Local
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ID ATI_C
AC P1660
DT 01-AU
                                                                                                                                                                                                                                                                         YF09 METJA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 TAFLINKVPLPVDKLAPLP-LDNILPFMDPLKLLLKTLGISVEHLVEGLRKCVNELGPEA 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                 similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to the phenylalanyl-tRNA synthetase beta chain family. Subfamily 1.
-!- SIMILARITY: Contains 1 tRNA-binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50886; TRBD; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
Metal-binding; Magnesium; RNA-binding; tRNA-binding;
                                                                                                                                                            SEQUENCE FROM N.A.
MEDILINE-99120557; PubMed-9923682;
MEDILINE-99120557; PubMed-9923682;
All R.A., Ling L.-S.L., Moir D.T., King B.L., Brown B.D., Doig P.C.,
Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
                                                         Hel.cobacter pylori 199 (Campylobacter pylori 199).
Bacteria, Proteobacteria, Epsilonproteobacteria, Campylobacterales,
Hel.cobacteraceae, Helicobacter.
                                                                                                                                                                                                                                                                                                        "Genomic sequence comparison of two unrelated isolates of the human
                                                                                                                                                                                                                                                                                                                                                                                        diphosphate + L-phenylalanyl_tRNA(Phe).
-!- COFACTOR: Binds 2 magnesium ions per tetramer (By similarity)
-!- SUBUNIT: Tetramer of two alpha and two beta chains (By
                                                                                                                                                                                                                                                                                                                                                                     CATALYTIC ACTIVITY: ATP + L-phenylalanine + tRNA(Phe) = AMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRNA-BINDING.
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (VIA CARBONYL OXYGEN)
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAGNESIUM (BY SIMILARITY)
MAGNESIUM (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70BDAFD202FED425 CRC64;
Phenylalanyl-tRNA synthetase beta chain (EC 6.1.1.20) (Phenylalanine--tRNA ligase beta chain) (PherS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 67.5;
Pred. No. 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pheT bact; 1.
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38.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            744 NSAVQKALEIL 754
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PROSITE; PS50886; TRBD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79 SEAVKKLLEAL 89
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome.
                                                                                                                          NCBI_TaxID=85963;
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443
                                            OR JHP0979.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/amnounce/or send an email to license@ib-sib.ch).
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MEDLINE=85.29750; PubMed=2993999;
Dhaese P., Seurinck J., de Smet B., van Montagu M.;
Nucleotide sequence and mutational analysis of an immunity repressor gene from Bacillus subtilis temperate phage phi 105.";
Nucleic Acids Res. 13:5441-5455(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDLINE=86656972; PubMed=3934047;

Cully D.F., Garro A.J.;

"Nucleotide sequence of the immunity region of Bacillus subtilis

bacteriophage phi 105: identification of the repressor gene and its

mRNA and protein products.";

Gene 38:153-164(1985).

-!- SIMILARITY: Contains 1 HTH cro/C1-type DNA-binding domain.
                                                                                                                                                                                                                                                 van Kaer L., Gansemans Y., van Montagu M., Dhaese P.; "Interaction of the Bacillus subtilis phage phi 105 repressor DNA:
                                                                                                                          dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A33579; RPBRFS.
InterPro; IPR001387; HTH 3.
Ffam; PF01381; HTH 3.
Franscription regulation; Repressor; DNA-binding; Early protein.
Transcription regulation; Repressor; DNA-binding; Early protein.
ODMAIN
18 37 H-T-H WOITF (POTENTIAL).
SEQÜENCE 144 AA; 16520 MW; EEEDGEB3E4B34AIE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.8%; Score 68; DB 1; Length 144; 24.3%; Pred. No. 5.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 KDIAKRMEEIRKDLEKSDGLSFSGEPMSQEAVESLMEAMEHIV 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 LINKVPLPVDKLAPLPLDNILPFMDPLKLLLKTLGISVEHLV----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
    P06153; P15239;
01-07M-1988 (Rel. 06, Created)
01-PR-1990 (Rel. 14, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13; Mismatches
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                                                                                                                                                                                                        SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=88283656; PubMed=3135184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X02799; CAA26567.1; ALT_INIT.
EMBL; M11920; AAA88396.1; -.
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                                                                                  Immunity repressor protein.
Bacteriophage phi-105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                           genetic analysis.";
EMBO J. 7:859-866(1988)
                                                                                                                            Viruses; dsDNA viruse
Lambda-like viruses.
VCBI TaxID=10717;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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16-OCT-2001
16-OCT-2001
28-FEB-2003
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7;

27; Indels

Length 764;

DB 1;

Matches

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RESULT 9

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ProDom; PD029354; Mamgb/prostatn; 1.
PRCSITE; PS00403; UTEROGLOBIN_1; FALSE_NEG.
PRCSITE; PS00404; UTEROGLOBIN_2; 1.
                                                                                                                                                     Signal; Glycoprotein; Steroid-binding. SIGNAL
                                         PIR; A92395; BORT3.
InterPro; IPR003627; Mamgb/prostatn.
InterPro; IPR001329; Uteroglobin_subf.
InterPro; IPR006038; Uteroglobin_supf.
Pf01099; Uteroglobin; 1.
           EMEL; V01263; CAA24577.1; -. EMEL; M71245; AAA41965.1; -.
                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                             CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                   CAFBOHYD
                                                                                                                                                                                                   CHAIN
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                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBDATT: PROSTATEIN IS COMPOSED OF THREE DIFFERENT PEPTIDES CALLED C1, C2 AND C3. THESE FORM COVALENT C1:C3 (F) AND C2:C3 (S) HETERODIMERS WHOSE NONCOVALENT ASSOCIATION FORMS TETRAMERIC (C1:C3/C3:C2) PROSTATEIN MOLECULES.
                                                                                                                                                                                                                                                                MEDLINE-83082848; PubMed-6294095;
Parker M.G., White R., Hurst H., Needham M., Tilly R.;
"Prostatic steroid-binding protein. Isolation and characterization of
                                                                                                                                                                      Fattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 19-95.
MEDIATE-SHIBSTOS; PubMed=7014218;
MEDIATE-SHIBSTOS; PubMed=7014218;
MEDIATE-SHIBSTOS; PubMed=7014218;
MEDIATE-SHIBSTOS; PubMed=7014218;
"Structural studies on rat prostatic binding protein. The primary structure of its glycosylated component C3.";
EDLY. J. Biochem. 115:115-121(1981).
-!- FUNCTION: PART OF PROSTATEIN WHICH IS THE MAJOR SECRETORY GLYCOPPOTRIN OF VENTRAL PROSTATE GLAND. STEROID-BINDING PROTEIN;
CAN BIND NOW-POLAR STEROIDS, CHOLESTEROL AND A GROUP OF SMALL PROLINE-RICH PEPTIDES.
                                                                                                                                                                                                                                                                                                                                                                                                                        "Isolation of two genomic sequences encoding the Mr = 14,000 subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: VENTRAL PROSTATE.
-!- INDUCTION: ANDROGEN DEPENDENT, AS SHOWN BY THE DECREASE IN THE LEVEL OF THE PROTEIN POLLOWING.
-!- MISCELLANEOUS: C3 IS ENCODED BY TWO DIFFERENT GENES.
-!- SIMILARITY: Belongs to the uteroglobin family. Lipophilin
                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=83238526; PubMed=6190812;
Viskochil D.H., Perry S.T., Lea O.A., Stafford D.W., Wilson E.M.,
                                                                   P02780; Q63463;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Prostatic steroid-binding protein C3 chain precursor (Prostatein peptide C3):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tan J.A., Marschke K.B., Ho K.-C., Perry S.T., Wilson E.M., French F.S.;
"Response elements of the androgen-regulated C3 gene.";
J. Biol. Chem. 267:4456-4466 (1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tan J.A., Marschke K.B., Ho K.C., Perry S.T., Wilson E.M., French F.S.;
                                                              95 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                        of rat prostatein.";
J. Biol. Chem. 258:8861-8866(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biol. Chem. 267:7958-7958(1992).
                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=92218467; PubMed=1339454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=92165796; PubMed=1537831;
                                                                                                                                                                                                                                                                                                                   genes.";
Biol. Chem. 258:12-15(1983)
                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                    NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                              French F.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ERRATUM
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                                RESULT 10
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1 MKLVTIFLLVTISLCSY-SATAFLINKVPLPVDKLAPLPLDNILPFMDPLKLLLKTL-GI

59 SVEHLVEGLRKCVNELGPEASEAVKKLLEAL 89

8;

37; Indels

Score 67; DB 1; Length 95; Pred. No. 4.4;

14.6%; Sco. No. 27.5%; Pred. No. 27.5%; Mismatches

25; Conservative

F7F7F1A0C882E375 CRC64; N-LINKED (GLCNAC. .). D -> A (IN REF. 3). G -> S (IN REF. 2).

10730 MW;

35 53

PROSTATIC STEROID-BINDING PROTEIN C3

18 95

13

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                                                                                                                             30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
acetylmuramoylalanine--D-glutamate ligase (EC 6.3.2.9) (UDP-N-accetylmuramoyl-L-alanyl-D-glutamate synthetase) (D-glutamic acid
                                                                                                                                                                                                                                                                                                                                                                                      Andersson S.G.E., Zomorodipour A., Andersson J.O., Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K., Eriksson A.-S., Winkler H.H., Kurland C.G.; "The genome sequence of Rickettsia prowazekii and the origin of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 366:133'140(1998).
-!- FUNCTION: Cell wall formation. Catalyzes the addition of glutamate to the nucleotide precursor UDP-N-acetylmuramoyl-L-
                                                                                                                                                                                                                                                    Ricketteia prowazekii.
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                 445 AA.
FTEKAVKQFKQCFLDQTDKTLENVGVMMEAI
                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                         STRAIN-Madrid E;
MEDLINE-99039499; PubMed-9823893;
                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                         adding enzyme).
                                                                                                                                                                                                                                                                                                          NCBI_TaxID=782;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mitochondria."
                                                                                                                                                                                                                                       MURD OR RP410.
                                                                                                  RICPR
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                                                                                                                                                                                                                                                                                                                                                                                                    6 IFLLV----TISLCSYSATAFLINKVPLPVDKLAPLPLDNILPFMDPLKLLLKTLGISVE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22388257; PubMed=12477932; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.L., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Singh G., Katyal S.L., Brown W.E., Phillips S., Kennedy A.L., Anthony J., Squeglia N., "Amino-acid and cDNA nucleotide sequences of human Clara cell 10 kDa
                                                                                                                                                                                                                                                                                                                                                                    30; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hay J.G., Danel C., Chu C., Crystal R.G.;
"Human CC10 gene expression in airway epithelium and subchromosomal locus suggest linkage to airway disease.";
Am. J. Physiol. 268:L565-L575(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PI1684: Q9UCM2, Q9UCM4, 010-0CT-1989 (Rel. 12, Last sequence update) 01-0CT-1989 (Rel. 12, Last sequence update) 10-0CT-2003 (Rel. 42, Last annotation update) clara cell phospholipid-binding protein precursor (CCPBP) (Clara 10 kba secretory protein) (CCLO) (Uteroglobin) (Urine protein 1) (UP1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                       HAMAP, MF_00639; -; 1.
HAMAP, MF_00639; -; 1.
InterPro; IPR000713; Mur_ligase.
InterPro; IPR004101; Mur_ligase_C.
InterPro; IPR010101; Mur_ligase_C.
InterPro; IPR0125; Mur_ligase; 1.
Pfam; PF02875; Mur_ligase; 1.
IGRFAMs; IGR01087; murD; 1.
IGRFAMs; Complesis; Cell wall; Cell division; Ligase; ATP-binding; Complete proteon ATP (POTENTIAL).
NP_BIND
                                                                                                                                                                                                                                                                                                                               Length 445;
                                                                                                                                                                                                                                                                                                                                                                    24; Indels
                                                                                                                                                                                                                                                                                               50129 MW; B9CCCF7437FB7AA6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 HLVEGLRKCVNELGPEASEAV-----KKLLEALS 90
                                                                                                                                                                                                                                                                                                                             14.6%; Score 67; DB 1;
32.0%; Pred. No. 22;
iive 12; Mismatches 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochim. Biophys. Acta 950:329-337(1988).
 entities requires a license agreement (Se or send an email to license@isb-sib.ch).
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TISSUE=Lung;
MEDLINE=89000784; Pubmed=3167058;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCGBIAL OR UGB OR CC10 OR CCSP.
                                                     EMBL; AJ235271; CAA14867.1; -.
                                                                                                                                                                                                                                                                                                                                                                     31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Human)
                                                                      PIR; A71699; A71699.
HSSP; P14900; 1UAG.
                                                                                                                                                                                                                                                                                               445 AA;
                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bossik S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Pahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length
Thuman and mouse cDNA sequences.",
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Umland T.C., Swaminathan S., Singh G., Warty V., Furey W.,
Pletcher J., Sax M.,
Sax M.,
Sax M.,
Structure of a human clara cell phospholipid-binding protein-ligand
complex at 1.9-A resolution.";
Nat. Struct. Biol. 1:538-545(1994).
INT. Struct. Biol. 1:538-545(1994).
POLYCHIONI BINDS PHOSPHAIDYLCHOLINE, PHOSPHATIDYLINOSITOL,
POLYCHIORINATED BIPHENILS (PCB) AND WEAKLY PROGESTERONE, POTENT
INHIBITOR OF PHOSPHOLIPASE A2.
                                                                                                                                                                                                                                                                                                                                                     [4] SEQUENCE OF 1-18 FROM N.A. SEQUENCE OF 1-18 FROM N.A. WEDLINE=53250776; PubMed=1284526; Wolf M., Klug J., Hackenberg R., Gessler M., Grzeschik K.-H., Beato M., Suske G.; "Human CCIO, the homologue of rabbit uteroglobin: genomic cloning, chromosomal localization and expression in endometrial cell lines."; Hum. Mol. Genet. 1:371-378(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bernard A., Roels H., Lauwerys R., Witters R., Gielens C., Soumillion A., Van Damme J., De Ley M.; "Human urinary protein 1: evidence for identity with the Clara cell protein and occurrence in respiratory tract and urogenital
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECUENCE OF 22-74.
TISSUB-UTINE;
MELINE=93016476; PubMed=1400743;
Okutani R., Itoh Y., Hirata H., Kasahara T., Mukaida N., Kawai T.;
Okutani R., Itoh Y., Hirata H., Kasahara T., Mukaida I.;
Simple and high-yield purification of urine protein 1 using
imunoafithinty chromatography: evidence for the identity of urine
protein 1 and human Clara cell 10.kilodalton protein.";
J. Chromatogr. A 577:25-35(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: Homodimer; antiparallel disulfide-linked.
TISSUE SPECIFICITY: Clara cells (nonciliated cells of the
surface epithelium of the pulmonary airways).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: Belongs to the uteroglobin family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=93009001; PubMed=1395029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clin. Chim. Acta 207:239-249(1992)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rissum=Urine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    secretions.";
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MEDLINE=91358323; PubMed=1885524;
MEDLINE=91358323; PubMed=1885524;
Byans D.J., Jones R.L., Woodley P.R., Wilborn J.R., Robson R.L.;
"Nuclectide sequence and genetic analysis of the Azotobacter chroococcum nifUSVWZM gene cluster, including a new gene (nifP) which encodes a serine acetyltransferase.";
J. Bacteriol. 173:5457-5463(1991).
-!- FUNCTION: CATALYZES THE REMOVAL OF ELEMENTAL SULFUR ATOMS FROM CYSTEINE TO PRODUCE ALANINE. SEEMS TO PARTICIPATE IN THE BIOSYNTHESIS OF THE NITROGENASE METALLOCLUSTERS BY PROVIDING THE INDREANIC SULFUR REQUIRED FOR THE FE-S CORE FORMATION (BY SIMILARITY).
                                                                                                                                                                                                                                                    CLARA CELL PHOSPHOLIPID-BINDING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                  31; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales,
Pseudomonadaceae, Azotobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Cysteine desulfurase (EC 4.4.1.-) (Nitrogenase metalloclusters
                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 91;
                                                                                                                                                                                                                                                                                                                                                                                 30; Indels
                                                                                                                                                                                                                                                                                R -> G (in dbSNP:1802624).

/FIId=VAR 012045.

T -> A (in dbSNP:1802632).

/FIId=VAR 012046.

C -> E (IN REF. 7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 EHLVE------GLRKCVNELGPEASEAVKKLLEALS 90
                                                                                                                                                                                                                                                             (WITH C-90).
(WITH C-24).
                                                                                                                                                                                                                                                                                                                                       FE65ACA678F12ABD CRC64;
                                                                                                                  InterPro; IPR006039; Utergl.
InterPro; IPR006039; Utergl.
InterPro; IPR000329; Utercglobin sub.
InterPro; IPR006039; Utercglobin subf.
InterPro; IPR006038; Utercglobin supf.
Pfam; PF01099; Utercglobin; 1.
PRINTS; PR00466; UTERCGLOBIN.
ProDom; PD012475; Utercglbn_sub; 1.
PROSITE; PS00404; UTERCGLOBIN 1; 1.
PROSITE; PS00404; UTERCGLOBIN 1; 1.
PROSITE; PS00404; UTERCGLOBIN 1; 1.
Phospholipase A2 inhibitor; Signal; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                             Score 66.5; DE pred. No. 4.7; 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            395 AA
                                                                                                        GO; GO:0007566; P:embryo implantation; TAS.
                                                                                                                                                                                                                                                               INTERCHAIN
                              EMBL; BC004401; AAH04401.1; -... EMBL; X59075; CAA42532.1; -... PIR; JS0036; JS0036. PIR; S26651; S2651. HSSP; PO2779; 1UTG. Genew; HGNC:12523; SCGBIA1.
                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1991 (Rel. 20, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Azotobacter chroococcum mcd 1.
                                                                                                                                                                                                                                                                                                                                                             14.5%;
 X13197; CAA31584.1; -.
UO1101; AAA81885.1; -.
UO1102; AAA18297.1; -.
                                                                                                                                                                                                                                                                                                                                         91 AA; 9994 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           biosynthesis protein nifS)
                                                                                                                                                                                                                                                                                                                                                                                  26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                    91
24
90
56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=355;
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24
90
56
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P23120;
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                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                             CONFLICT
                                                                                                                                                                                                                                                                                                                                                             Query Match
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                      EMBL;
                                                                                             MIM;
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                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 ISLCSYSAT-AFLINKVPLPVDKLAPLPLDNILPFMDPLKLLLKTLGISVE----HLVEG 66
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STRAINS-JAL-1 / DSW 2661 / ATCC 43067;

BUIL C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Surton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-E., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Wosse C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
-!- COFACTOR: Pyridoxal phosphate (By similarity).
-!- SUBUNIT: Homodimer (By similarity).
-!- SIMILARITY: Belongs to class-V of pyridoxal-phosphate-dependent aminotransferases. Nifs/iscS subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY.
PYRIDOXAL PHOSPHATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY. 909F70995B312BDA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.5%; Score 66.5; DB 1; 28.9%; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000192; Aminotrans V.
Pfam; PF00266; aminotran 5; 1.
PRCSITE; PS00595; AA TRANSFER CLASS 5; 1.
Nitrogen fixation; Lyase; Pyridoxal phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-WAR-2004 (Rel. 43, Created)
15-WAR-2004 (Rel. 43, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Hypothetical protein MJ1321.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            713 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 273:1058-1073(1996).
-!- SIMILARITY: Contains 1 Piwi domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : : : | | : | : | | 158 MARMADEAGIMFHTDAVQAVRKL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 LRKCVNELG----PEASEAVKKL 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      318 318 B)
395 AA; 43165 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMEL; M60090; AAA22160.1; -. PIR; B43706; B43706.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Methanococcus jannaschii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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318
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Best Local Similarity
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                                                                                                                                                                                                   ۲;
                                                                                                                                                                                                                                               25 NKVPLPVDKLAPLPLDNILPFMDPLKLLLKTLGISVEHLVEGLRKCVNELGPBASEAVKK 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypophthalmichthys molitrix (Silver carp).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi;
Actinopterygii, Neopterygii, Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Hypophthalmichthys.
                                                                                                                                                                                                   13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chang Y.S., Huang F.-L., Lo T.B.;
"Molecular cloning of silver carp and bighead carp prolactin.";
"Gen. Comp. Endocrinol. 87:260-255(1992).
-!- SUBCELLILLAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Pituitary glands.
-!- SIMILARITY: Belongs to the somatotropin/prolactin family.
                                                                                                                                                                        DB 1; Length 713;
                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 BY SIMILARITY.
207 PROLACTIN.
180 BY SIMILARITY.
207 BY SIMILARITY.
23033 MW; E8302AA6855FC64D CRC64;
                                                                                                                                           713 AA; 84582 MW; EB0B3265C600DF2D CRC64;
                                                                                                                                                                     / Match 14.5%; Score 66.5; DB 1; I
Local Similarity 24.6%; Pred. No. 39;
hes 15; Conservative 14; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-FIBS-2003 (Rel. 41, Last annotation update)
Prolactin precursor (PRL) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                            207 AA.
                                             PIR; no...
TIGR; MJ132;
InterPro; IPR003165; Piwi.
Pfam; PF02171; Piwi; 1.
PR0SITE; PS50822; PIWI; 1.
Hypothetical protein; Complete proteome.
A26 699 PTWI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, X61052; CAA43386.1; -. PIR; S21365; S21365. HSSP, Q28632; 1AN3. InterPro; IPR001400; Somatotropin. Ffam; PP00103; hormone; 1. PRNINF; PR0035; SOMATOTROPIN. PROSITE; PS00366; SOMATOTROPIN 1; 1. PROSITE; PS00338; SOMATOTROPIN 1; 1.
or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Pituitary;
MEDLINE=93012875; PubMed=1398019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pituitary; Signal
                           EMBL; U67572; AAB99334.1;
PIR; H64464; H64464.
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21
21
66
197
207 AA;
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123 I 123
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DISULFID
SEQUENCE
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NON TER
                                                                                                                                                                        Query Match
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                                                              69
                                                              13 SLCSYSATAFLINK---VPLPVDKLAPLPLDNILPFMDPLKLLLKTLGISVEHLVEGLRK
                                Gaps
                              7;
 Length 207;
                              Indels
                                42;
 DB 1;
14.3%; Score 65.5; Di
26.2%; Pred. No. 14;
tive 13; Mismatches
                                                                                                                                                 70 CVNELGPEASEAVKKLLEALSHLV 93
                                                                                                                                                                                                              2, 2004, 20:19:33
                                 Conservative
                Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                              Search completed: June
Job time: 4.6175 secs
 Query Match
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Н

GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd. Copyright

- protein search, using sw model OM protein

Run on:

(without alignments) 1413.099 Million cell updates/sec June 2, 2004, 20:14:10 ; Search time 6.33063 Seconds

US-09-700-770-7

459 1 MKLVTIFLLVTISLCSYSAT......LGPEASEAVKKLLEALSHLV 93 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 283366 segs, 96191526 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

summaries

Database :

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		*			SUMMARIES	
Result No.	Score	Query Match	Query Match Length	DB	ID	Description
1	78.5	17.1	2109	t	T31352	hypothetical prote
2	72	15.7	153		D64488	
e	70	S	1502		T48309	-
4	69.5	15.1	425	7	H90415	ical
D.	69.5	ß	451		A96920	ABC
9	69.5	ഗ	206		F85016	
7	69.5	'n.	268		E97066	membrane associate
80	68.5	4.	335		T05268	hypothetical prote
o,	68.5	14.9	356		D85406	hypothetical prote
10	68.5	4.	464		T47710	glucuronosyl trans
11	68.5	4.	1284		WMVZAI	A-type inclusion p
12	68	14.8	147		RPBPFS	immunity repressor
13	68	14.8	239		D70359	conserved hypothet
14	68	4.	693		C86364	hypothetical prote
15	67.5	14.7	512		A86238	protein F14N23.31
16	67.5	•	266		AD0816	nitrate/nitrite se
17	67.5		764		F71863	phenylalanine-tRNA
18	67	14.6	95	Н	BORT3	prostatic steroid-
19	67		445	N	A71699	UDP-n-acety1muramo
20	66.5		91	~	JS0036	Clara cell 10K pro
21	66.5		128	7	T15017	hypothetical prote
22	66.5	14.5	396	7	B43706	nitrogenase cofact
23	66.5	14.5	713	~	H64464	
24	99	14.4		7	F96565	Н
25	99	14.4		N	G75179	
26	99	14.4	793	N	C83260	hypothetical prote
27	99	14.4	983	Ŋ	H72510	
28	9	14.4	2471	~	T42977	large tegument pro
29	65.5	14.3	192	7	F72559	hypothetical prote

prolactin - silver HmsT protein limbo	phosphodiesterase	protein kinase (EC	creatine kinase BH	probable transcrip	diaminopimelate de	toxin secretion AT	protein K07E3.6 [i	methyl-accepting c	cobalamin-independ	protein F54D8.1 [i	hypothetical prote	DNA ligase [import	hypothetical prote	NADH dehydrogenase
S21965	153865	853538	F83662	T37111	F82360	H82381	H89582	C70174	AD1656	H88449	T20929	G89978	T15920	Н90622
04.0	1 (1	Н	N	N	N	~	~	7	7	7	~	7	N	7
207	844 444	308	356	384	417	704	964	715	765	1120	432	667	669	116
14.3	14.3	14.2	14.2	14.2	14.2	14.2	14.2	14.1	14.1	14.1	13.9	13.9	13.9	13.8
65.5	65.5	65	65	65	65	65	65	64.5	64.5	64.5	64	64	64	63.5
30	35	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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hypothetical protein - Pelargonium x hortorum
C;Species: Pelargonium x hortorum
C;Species: Pelargonium x hortorum
C;Species: Pelargonium x hortorum
C;Species: Desp-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000
C;Accession: T31352
R;Downie, S.R.; Katz-Downie, D.S.; Wolfe, K.H.; Calie, P.J.; Palmer, J.D.
Curr. Genet. 25, 367-378, 1994
A;Title: Structure and evolution of the largest chloroplast gene (ORF2280): internal
A;Reference number: Z21012; MUID:94363755; PMID:8082181
A;Reference number: Z21012; MUID:94363755; PMID:8082181
A;Reference type: DNA
A;Residues: 1-2109 < DOW>
A;Residues: 1-2109 < DOW>
A;Cross-references: EMBL:MB3200; NID:9468913; PID:9468914; PIDN:AAA73173.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 2109;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24;
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Best Local Similarity 24.0%; Pred. No. 13;
Matches 23; Conservative 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
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3, 622 46

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623 IRIYELKGPTVQPCNPLLESIGLQILHL-NKLKPCL 657 -----DPLKLLLKTLGISVEHLVEGLRKCV 71 ò g

47

Cypothetical protein MJI509 - Methanococcus jannaschii Cypothetical protein MJI509 - Methanococcus jannaschii Cypothetical Brotein MJI509 - Methanococcus jannaschii Cypothetical Species: Methanococcus jannaschii Cypothetis I3-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000 Cyaccession: D64488 Fishult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blab Reich, C.I.; Overbeek, R.; Kirkness, B.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, Schence 273, 1058-1073, 1996 A.T. Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996 A.Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese A.T. Change anome sequence of the methanogenic archaeon, Methanococcus jannasca, A.R. Reference number: A64300; WUID:96337999; PMID:8688087

A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-153 <BUL>

A; Cross-references: GB:U67592; GB:L77117; NID:g2826425; PIDN:AAB99534.1; PID:g1500398 C; Genetics: A; Map position: FOR1482026-1482487

Length 153;

15.7%; Score 72; DB 2; 28.8%; Pred. No. 3.8; Query Match Best Local Similarity

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probable RING zinc finger protein [imported] - Arabidopsis thaliana cyprobable RING zinc finger protein [imported] - Arabidopsis thaliana (c) protein [c) bate: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 17-May-2002 C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 17-May-2002 C; Accession: F85016 R; anonymous, The Buropean Union Arabidopsis Genome Sequencing Consortium, The Cold S Nature 402, 769-777, 1999 A; Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana. A; A; Reference number: A85001, MUID:20083488; PMID:10617198 A; A; Astus: prefilminary A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-506 <STO>
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross.references: GB:AE001437; PIDN:AAK78148.1; PID:g15022994; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            247 MSIAQIPIIL---LSVYSIEGILRHSIPEKILKLKKEKYSDDKIKLIALSNVYVSLKNLK 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69
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C;Superfamily: Arabidopsis thaliana hypothetical protein A_IG002N01.19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 15.1%; Score 69.5; DB 2; Length 5 Best Local Similarity 31.4%; Pred. No. 24; Matches 27; Conservative 15; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
15.1%; Score 69.5; DB 2;
Best Local Similarity 28.4%; Pred. No. 21;
Matches 21; Conservative 14; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MKLVTIFLLVTISLCSYSATAFLINKVPLPV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          239 C-NQLGRGEARSSEKLEKALEKIEKL 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70 CVNELG---PEASEAVKKLLEALSHL 92
                            186 PGQYEVKLSQKPVLEAADSLI 206
P---EASEAVKKLLEALSHLV 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    || || || ::
304 FLLITLVISIEGIL 317
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       92
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A;Reference number: A99139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Map position: 5
A;Introns: 216/3; 253/3; 292/3; 345/3; 399/3; 449/3; 490/2; 854/3; 1248/3; 1325/3; 1360/
A;Note: F9G14.190
                                                                                                                                                                                                                                                                                                 hypothetical protein F9G14.190 - Arabidopsis thaliana (S.Species Arabidopsis thaliana (mouse-ear cress) (S.Species 120-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000 (S.Accession: T48309 "N. Tarryn, N., Ardiles, W.; Buysshaert, C.; Dasseville, R.; De Clerck, R.; De ewes, H.W.; Rudd, S.; Lencke, K.; Mayer, K.F.X. submitted to the Protein Sequence Database, April 2000
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A;Molecule type: DNA
A;Residues: 1-425 <KUR>
A;Cross-references: GB:AE006641; NID:g13815744; PIDN:AAK42583.1; GSPDB:GN00155
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                                                 22 FLINKVPLPVDKLAPLPLDNILPFMDPLKLLKTLGISVEHLVEGLRKCVNELGPEASEA 81
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       8; Gaps
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       Indels
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A,Molecule type: DNA
A,Residues: 1-1502-282>
A,Cross-references: EMBL:AL162973
A,Experimental source: cultivar Columbia; BAC clone F9G14
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       22;
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15.3%; Score 70; DB 2
Best Local Similarity 22.6%; Pred. No. 68;
Matches 19; Conservative 19; Mismatches
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15.1%; Score 69.5; D
Best Local Similarity 30.9%; Pred. No. 20;
Matches 25; Conservative 13; Mismatches
         17; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 RKCVNELGPEASEAVKKLLEALSH 91
           Conservative
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A;Accession: T48309
                                                                                                                                                                      ||:|:
145 AKKVLD 150
                                                                                                                                           82 VKKLLE 87
           19;
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A;Gene: glnA-2
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           Matches
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C;Accession: T47710
R;Benes, V.; Murmbach, E.; Drzonek, H.; Ansorge, W.; Mewes, H.W.; Lemcke, K.; Mayer,
submitted to the Protein Sequence Database, March 2000
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A,Residues: 1-1284 <FUN>
A;Residues: 1-1284 <FUN>
A;Cross-references: GB:D00319; NID:g221140; PIDN:BAA00222.1; PID:g221141
A;Cross-references: GB:D0.2 Pickup, D.J.
EMBO J. 6, 3787-3794, 1987
A;Title: Messenger RNAs of a strongly-expressed late gene of cowpox virus contain A;Reference number: S01494; MUID:88111568; PMID:2828037
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C;Species: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 16-Jun-2000
C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 16-Jun-2000
C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 16-Jun-2000
R;Punahashi, S.; Sato, T.; Shida, H.
J;Gen. Virol. 69, 35-47, 1988
A;Title: Cloning and characterization of the gene encoding the major protein of A;Reference number: JQ0006; MUID:88089536; PMID:2826668
                                   A;Residues: 1.356 <STO>
A;Cross-references: GB:NC_001268; NID:g7270398; PIDN:CAB80165.1; GSPDB:GN00140
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          glucuronosyl transferase-like protein - Arabidopsis thaliana
N;Alternate names: protein F1116.120
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 19-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 SLCSYSATAFLINKVPLPVDKLAPLPLDNILPFMDPLKLLLKTLGISVEHLVEGLRKCVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 464;
                                                                                                                                                                                                                                                                                                                                                                        Length 356;
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40.0%; Pred. No. 21;
tive 10; Mismatches
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30.6%; Pred. No. 28;
ative 15; Mismatches
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                                                                                                                                                                                 A,Gene: A14934480
A,Map position: 4
C,Superfamily: beta-1,3-glucanase
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Best Local Similarity 40.0%;
Matches 20; Conservative 1
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Matches 22; Conserv
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A, Molecule type: DNA
A, Residues: 1-109 <PAT>
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A, Status: preliminary
A, Molecule type: DNA
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A; Note: F1116.120
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C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 02-Mar-2001
C; Accession. D85406
R; Anonymous, The Buropean Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin Nature 402, 769-777, 1999
N; Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A; Reference number: A88001; MUID: 20083488; PMID: 10617198
                                        Cispecies: Clostridium acetobutylicum
Cispecies: Clostridium acetobutylicum
Cibate: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
Cibate: 14-Sep-2001 #sequence_revision 14-Sep-2001
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membrane associated chemotaxis sensory transducer protein (MSP domain and HAMP domain)
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: T05268
R;Bevan, M.; Terryn, N.; Ardiles, W.; Buysshaert, C.; Dasseville, R.; De Clerck, R.; Evevan, M.; Terryn, N.; Ardiles, W.; Buysshaert, C.; Dasseville, R.; De Clerck, R.; Steference number: Z15406
A;Reference number: Z15406
A;Recession: T05268
A;Residues: 1-335 < BEV>
A;Residues: 1-335 < BEV>
A;Cession: EMBL,AL023094
A;Experimental source: cultivar Columbia; BAC clone T4L20
C;Genetics:
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A Modecule type: DNA
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A Medicule type: DNA
A Modecule type: DNA
A Modecu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 335;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 NILPEMDPLKLLLKTLGISVEHLVEGLRKCVNELGPEASEAVKKLLEALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---EAVKKLLEALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.1%; Score 69.5; DB 2; 24.8%; Pred. No. 27; tive 19; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.9%; Score 68.5; Dilarity 40.0%; Pred. No. 20; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     I---SVEHLVEGLRKCVNELGPEAS
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A, Note: intron positions not resolved
A, Note: T4L20.60
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C, Superfamily: beta-1, 3-glucanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 20; Conserv
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hes 27; Conserv
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hypothetical protein F19G10.4 [imported] - Arabidopsis thaliana Cispecies: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 19-Apr-2002
C;Accession: C86564
R;Theologis A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alochin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, M.F.; Hudghes, B.; Haizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzi, Rizzo, M.; Rooney, T.; Rowhey, D.; Sakano, H.; Southwick, A.M.; Sun, H.; Tall Rizzo, M.; Woney, T.; Rohwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tall Rytitle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Resedus: preliminary
A;Residus: 1-63 strong A;Residus (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) strong (A) stron
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A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: D70359
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-239 <AQF>
A;Crose-references: GB:AE000701; NID:92983260; PIDN:AAC06868.1; PID:92983274; GB:AE0
A;Experimental source: strain VF5
                                                                                                                            C;Species: Aguifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
C;Accession: D70359
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AE005172; NID:g2462833; PIDN:AAB72168.1; GSPDB:GN00141
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 LVTISLC--SYSATAFLINKVPLPVDKLAPLPLDNILPFMDFLKLLLKTLGISVEHLVEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 IFLL-VIISLCSYSATARLINK-----VPLPVDKLAPLPL----DNILPFMDPL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50 ----KILLKTLGISVEHLVEGLRKCVNELGPEAS--EAVKKLLEALS 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 14.8%; Score 68; DB 2; Length 693; 1. Similarity 31.8%; Pred. No. 48; 34; Conservative 14; Mismatches 37; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27; Indels
                                                                                                         conserved hypothetical protein aq 674 - Aquifex aeolicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , Match 14.8%; Score 68; DB Local Similarity 32.6%; Pred. No. 15; He 28; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 LRKC-----VNELGPEASEAVKKLLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Map position: 1
C;Superfamily: ferric reductase FRE2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 34
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A, Gene: aq_674
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Matches
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*Residues: 1-147 <CUL.>

R,van Kaer, L.; Gansemans, Y.; van Montagu, M.; Dhaese, P.

EMBO J. 7, 859-866, 1988

*A,Title: Interaction of the Bacillus subtilis phage phil05 repressor with operator DNA:

A,Reference number: S02459; MUID:88283656; PMID:3135184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Title: Nucleotide seguence and mutational analysis of an immunity repressor gene from A,Reference number: A93579; MUID:85297750; PMID:2993999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus subtilis bacteriophage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5
                                                                                                                                                                                                                                                                     24 LAEKANLSRSYLADIERDRYNPSLSTLEAVAGALGIQVSAIVGEETLIKEEQAEYNSKEE 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             change 16-Jun-2000
                                                                                                                                                                                                                                  30 PVDKLAPLPLDNIL---PFMDP--LKLLLKT-LGIS-----VEHLVEGLRKCVNELG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Cross-references.

A,Cully, D.F.; Garro, A.J.

A,Cully, D.F.; Garro, A.J.

A,Title: Nucleotide sequence of the immunity region of Bacillus subtilish A,Reference number: A91535, MUID:86056972; PMID:3934047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32;
                                                                                                                                                                          17;
                                                                                                                      Length 1284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.8%; Score 68; DB 1; Length 147; 24.3%; Pred. No. 9.2; tive 13; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84 XDIAKRMEEIRKDLEKSDGLSFSGEPMSQEAVESLMEAMEHIV 126
                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunity repressor protein - Bacillus phage phi-105
C;Species: Bacillus phage phi-105
A;Note: Bacillus subtilis
C;Date: 31-Mar-1988 #sequence revision 31-Mar-1988 #text_cha
C;Accession: A93579; A91535; S02459; T13543; A44339; A24521
R;Dhaese, P; Seurinck, J; De Smet, B; Van Montagu, M.
Nucleic Acids Res. 13, 5441-5455, 1985
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                                                                                                                                                                          24;
                                                                                                                      DB 1;
A;Cross-references: EMBL:X06343
C;Superfamily: cowpox virus A-type inclusion protein
C;Keywords: inclusion protein
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A;Status: prellminary; translated from GB/EMBL/DDBJ
A;Molecule type: DA
A;Residues: 4-147 <KOB>
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                                                                                                            Score 68.5; DB Fred. No. 82; 7; Mismatches
                                                                                                                   14.9%;
ilarity 36.0%;
Conservative '
                                                                                                                                                                                                                                                                                                                                                                                                    424 EYKTELEEAKRKLTE 438
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Best Local Similarity
Matches 25; Conserv
                                                                                                               Query Match
Best Local Similarity
Matches 27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-147 <DHA>
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RESOLY 15

AR6238

protein F14N23.31 [imported] - Arabidopsis thaliana
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 02-Mar-2001
E; Accession: A86238
R; Theologis, A. P. Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jankins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Schantz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719; PMID:11130712
A; Rocession: A86238
A; Cross-references: GB:AE005172; NID:94914345; PIDN:AAD32893.1; GSPDB:GN00141
C; Genetics:
A; Map position: 1
A; Map position: 1
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Best Local Similarity 32.8%; Pred. No. 39;
Matches 19; Conservative 8; Mismatches 16; Indels 15; Gaps
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Search completed: June 2, 2004, 20:22:20 Job time: 8.33063 secs

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US-10-187-883-244
US-10-194-363-244
US-10-194-460-244
US-10-194-463-244
US-10-194-484-2244
US-10-195-884-244
US-10-195-884-244
US-10-195-895-244
US-10-195-757-244
US-10-196-755-244
US-10-197-704-244
US-10-197-704-244
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US-10-199-313-244
US-10-199-313-244
US-10-202-413-244
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APPLICANT: ZABAG ZEMIN

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R.C513

CURRENT APPLICATION NUMBER: US/10/206,915

CURRENT PILING DATE: 2002-01-15

PRIOR PILING DATE: 2002-01-15

PRIOR PILING DATE: 1997-09-18

PRIOR PILING DATE: 1997-10-24

PRIOR PILING DATE: 1997-10-28

PRIOR PILING DATE: 1997-10-28

PRIOR PILING DATE: 1997-10-28

PRIOR PILING DATE: 1997-10-28
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APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Deenoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Goddowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
2, 2004, 20:19:10 ; Search time 16.5802 Seconds (without alignments) 1578.054 Million cell updates/sec
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US-10-199-670-244
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US-10-208-024-244
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US-10-176-483-244
US-10-176-1483-244
US-10-176-915-244
US-10-176-915-244
US-10-176-915-244
US-10-180-914-244
US-10-180-550-244
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Length 93;

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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P4430R1C401
CURRENT APPLICATION NUMBER: US/10/199,670
CURRENT FILING DATE: 2002-07-19
PRIOR APPLICATION NUMBER: 60/05263
PRIOR APPLICATION NUMBER: 60/05266
PRIOR APPLICATION NUMBER: 60/05266
PRIOR APPLICATION NUMBER: 60/05266
PRIOR APPLICATION NUMBER: 60/05266
PRIOR PILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-0-17
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-10-24
PRIOR PELING DATE: 1997-10-24
PRIOR PELING DATE: 1997-10-24
PRIOR PELING DATE: 1997-10-28
PRIOR PELING DATE: 1997-10-28
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           PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION UNDBER: 60/063544
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION data: 1997-10-28
Prior Application data removed - See File Wrapper or PALM.
UNDBER OF SEQ ID NOS: 612
SEQ ID NO 244
LENGTH: 93
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Pred. No. 2.3e-44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 244, Application US/10199670 Publication No. US20040033560A1 GENERAL INFORMATION:
APPLICANT: Baker Kevin P.
APPLICANT: Chen, Jian
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Wood, William I.
Zhang, Zemin
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Best Local Similarity 100.v
Local Similarity 100.v
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Smith, Victoria
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Goddard, Audrey
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; ORGANISM: Homo Sapien
US-10-199-670-244
                                                                                                                                                                                                  TYPE: PRT
CORGANISM: Homo Sapien
US-10-206-915-244
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US-10-199-670-244
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APPLICANT:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C464
CURRENT APPLICATION NUMBER: US/10/201,858
CURRENT PILING DATE: 2002-01-15
PRIOR PELICATION NUMBER: 10/652586
PRIOR PLICATION NUMBER: 60/059263
PRIOR APPLICATION NUMBER: 60/059266
PRIOR PLING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-01-17
PRIOR PAPLICATION NUMBER: 60/062250
PRIOR PLING DATE: 1997-10-24
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
PRIOR APPLICATION NUMBER: 60/063121
PRIOR APPLICATION NUMBER: 60/063140
PRIOR PELING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063441
PRIOR PELING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063541
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100.0%; Pred. No. 2.3e-44;
iive 0; Mismatches 0;
100.0%; Score 459; DB 12;
100.0%; Pred. No. 2.3e-44;
tive 0; Mismatches 0;
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    Sequence 244, Application US/10201858
    Publication No. US20040038337A1

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Watanabe, Colin K.
Wood, William I.
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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ORGANISM: Homo Sapien
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APPLICANT: Watenabe, Colin K.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C519
CURRENT PELICATION NUMBER: US/10/205,890
CURRENT FILING DATE: 2002-07-26
PRIOR PELICATION NUMBER: 00/05266
PRIOR APPLICATION NUMBER: 60/05926
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-10-17
PRIOR PELICATION NUMBER: 60/063120
PRIOR PELICATION NUMBER: 60/063120
PRIOR PELING DATE: 1997-10-24
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PRIOR FILING DATE: 1997-10-28
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Sequence 244, Application US/10205890 Publication No. US20040048334Al GENERAL INFORMATION:
APPLICANT: Baker Kevin P. APPLICANT: Chen, Jian
                                                                                                                                                                                                                                                                                                                                    Pan, James
Smith, Victoria
Watanabe, Colin K.
Wood, William I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 93; Conserv
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NS-10-208-024-244

Sequence 244, Application US/10208024

Publication No. US20040048335A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Chen, Jian

APPLICANT: Chen, Jian

APPLICANT: Goddard, Audrey

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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEWBRANE POLYFEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C538
CURRENT PELICATION NUMBER: US/10/208,024
CURRENT FILING DATE: 2002-01-15
PRIOR PELICATION NUMBER: 10/65268
PRIOR PELICATION NUMBER: 60/65263
PRIOR APPLICATION NUMBER: 60/65266
PRIOR APPLICATION NUMBER: 60/65266
PRIOR PELING DATE: 1997-09-18
PRIOR PELING DATE: 1997-09-18
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACLDS ENCODING THE SAME
FILE REPERENCE: P3430R1C465
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Wood, William I.
Godowski, Paul J.
Gurney, Austin L.
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Goddard, Audrey
Godowski, Paul J
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Best Local Similarity 100.
Matches 93; Conservative
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Smith, Victoria
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US-10-208-024-244
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R. FILING DATE: 1998-03-31
R. APPLICATION NUMBER: 60/080194
R. FILING DATE: 1998-03-31
R. APPLICATION NUMBER: 60/080327
R. FILING DATE: 1998-04-01
R. APPLICATION NUMBER: 60/080333
                                                                                                                                                                                                                                                                                                                                                                    R APPLICATION NUMBER: 60/063734
RR APPLICATION NUMBER: 60/063734
RR APPLICATION NUMBER: 60/063870
RR APPLICATION NUMBER: 60/064103
RR APPLICATION NUMBER: 60/065111
RR APPLICATION NUMBER: 60/065311
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R FILING DATE: 1997-11-24
R APPLICATION NUMBER: 60/066772
R FILING DATE: 1997-11-24
R FILING DATE: 1997-11-11
R FILING DATE: 1997-11-11
R APPLICATION NUMBER: 60/069135
R APPLICATION NUMBER: 60/069425
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APPLICATION NUMBER: 60/081049
FILING DATE: 1998-04-08
APPLICATION NUMBER: 60/081070
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FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/082568
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APPLICATION NUMBER: 60/079786
FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/080107
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FILING DATE: 1998-04-09
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APPLICATION NUMBER: 60/082569
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APPLICATION NUMBER: 60/082704
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APPLICATION NUMBER: 60/083322
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APPLICATION NUMBER: 60/068017
APPLING DATE: 1997-12-18
APPLICATION NUMBER: 60/077450
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APPLICATION NUMBER: 60/066120
FILING DATE: 1997-11-21
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APPLICATION NUMBER: 60/077649
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APPLICATION NUMBER: 60/078886
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APPLICATION NUMBER: 60/079664
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APPLICATION NUMBER: 60/069870
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APPLICATION NUMBER: 60/077632
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APPLICATION NUMBER: 60/063541
FILING DATE: 1997-10-28
APPLICATION NUMBER: 60/063544
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APPLICANT: Zhang-Zemin T.

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REPERBNCE: 1943 OR141

CURRENT APPLICATION NUMBER: US/10/174,581

CURRENT FILING DATE: 2002-06-18

PRIOR APPLICATION NUMBER: 60/059266

PRIOR APPLICATION NUMBER: 60/059266

PRIOR APPLICATION NUMBER: 60/059266

PRIOR APPLICATION NUMBER: 60/059266

PRIOR APPLICATION NUMBER: 60/062260

PRIOR PILING DATE: 1997-09-18

PRIOR PILING DATE: 1997-09-18

PRIOR PILING DATE: 1997-09-18

PRIOR PILING DATE: 1997-09-18

PRIOR PILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/062250

PRIOR PILING DATE: 1997-09-17

PRIOR PILING DATE: 1997-09-17

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      PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR FILING DATE: 2002-01-15
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR PILING DATE: 1997-09-18
PRIOR PAPLICATION NUMBER: 60/06256
PRIOR APPLICATION NUMBER: 60/06250
PRIOR PELING DATE: 1997-10-17
PRIOR PELING DATE: 1997-10-17
PRIOR PELING DATE: 1997-10-24
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PRIOR APPLICATION NUMBER: 60/063121
PRIOR PELING DATE: 1997-10-24
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Publication No. US20030017540A1
GENERAL INFORMATION:
CURRENT FILING DATE: 2002-07-23
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Gurney, Austin I.
Pan, James
Smith, Victoria
Watanabe, Colin K.
Wood, William I.
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APPLICANT: Chen, Jian
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul J
APPLICANT: Grane, Austin L
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanab. Colin
APPLICANT: Wood, William I.
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Goddard, Audrey
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ORGANISM: Homo Sapien
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PRIOR FILING DATE: 1938-04-28

FRIOR PLILING DATE: 1938-04-28

FRIOR APPLICATION NOWBER: 60/081496

FRIOR APPLICATION NOWBER: 60/081496

FRIOR APPLICATION NOWBER: 60/081499

FRIOR APPLICATION NOWBER: 60/081499

FRIOR APPLICATION NOWBER: 60/084414

FRIOR APPLICATION NOWBER: 60/084414

FRIOR APPLICATION NOWBER: 60/084639

FRIOR APPLICATION NOWBER: 60/08623

FRIOR PRILING DATE: 1998-65-12

FRIOR PRILING DATE: 1998-65-12

FRIOR PRILING DATE: 1998-65-13

FRIOR FILING DATE: 1998-65-13

FRIOR FILING DATE: 1998-66-13

FRIOR FILING DATE: 1998-66-14

FRIOR FILING DATE: 1998-66-15

FRIOR FILING DATE: 1
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3430R1C68
CURRENT APPLICATION NUMBER: US/10/176,483
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Prior application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
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100.0%; Score 459; DB 12;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
Matches 93; Conservative 0; Mismatches 0;
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PRIOR APPLICATION NUMBER: 60/08825
PRIOR APPLICATION NUMBER: 60/08826
PRIOR PLING DATE: 1998-06-10
PRIOR PLING DATE: 1998-06-10
PRIOR PLING DATE: 1998-06-11
PRIOR PILLING DATE: 1998-06-11
PRIOR PILLING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/08863
PRIOR PILLING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/08976
PRIOR PILLING DATE: 1998-06-12
PRIOR PELLING DATE: 1998-06-12
PRIOR PRILING DATE: 1998-06-12
PRIOR PELLING DATE: 1998-06-12
PRIOR PILLING DATE: 1998-06-12
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; Sequence 244, Application US/10176483
; Publication No. US20030017541A1
; GENERAL INFORMATION
APPLICATION NUMBER: 60/088824
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Best Local Similarity 100.0%;
Matches 93; Conservative 0;
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Smith, Victoria
Watanabe, Colin K.
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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US-10-176-483-244
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LENGTH: 93
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Desnoyers, Luc
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Godowski, Paul J.
Gurney, Austin L.
Pan, James
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Best Local Similarity 100.
Matches 93; Conservative
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Best Local Similarity 100.0
Matches 93; Conservative
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ORGANISM: Homo Sapien
                                TYPE: PRT
CORGANISM: Homo Sapien
US-10-175-914-244
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US-10-176-915-244
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 SEQ ID NO 244
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                     LENGTH: 93
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CURRENT APPLICATION NUMBER: US/10/176,914
CURRENT FILING DATE: 2002-06-20
Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: WOOD, WILLIAM II.
APPLICANT: SANG
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P343.0KLC76
CURRENT APPLICATION NUMBER: US/10/176,749
Prior application number: 2002-06-20
Prior application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
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Publication No. US20030017543A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
                                                                                                                                                                                       Sequence 244, Application US/10176749
Publication No. US20030017542A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
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Smith, Victoria
Watanabe, Colin K.
Wood, William I.
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Watanabe, Colin K.
Wood, William I.
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Godowski, Paul J.
Gurney, Austin L.
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Gurney, Austin L.
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Goddard, Audrey
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US-10-176-749-244
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US-10-176-914-244
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US-10-176-749-244
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LENGTH: 93
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430HCE: P3430HCE: P3420HCE: V3/10/176,915
CURRENT APPLICATION NUMBER: US/10/176,915
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100.0%; Score 459; DB 12;
100.0%; Pred. No. 2.3e-44;
Live 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                          ; Sequence 244, Application US/10176915; Publication No. US20030017544A1; GENERAL INFORMATION:
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Watanabe, Colin K.
Wood, William I.
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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RESULT 15
US-10-187-738-244
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Best Local
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CURRENT APPLICATION NUMBER: 105/10/180,550
CURRENT FILING DATE: 2002-06-25
            APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: ACOUNTS. ZECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430RLC64
CURRENT APPLICATION NUMBER: US/10/176,484
CURRENT FILING DATE: 2002-06-20
Prior application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
SEQ ID NO 244
LENGTH: 93
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 244
LENGTH: 93
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100.0%; Pred. No. 2.3e-44;
tive 0; Mismatches 0;
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Smith, Victoria
Watanabe, Colin K.
Wood, William I.
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Smith, Victoria
Watanabe, Colin K.
Wood, William I.
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Best Local Similarity
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ORGANISM: Homo Sapien
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, ORGANISM: Homo Sapien
US-10-176-484-244
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Best Local Similarity
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US-10-180-550-244
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APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C241
CURRENT PRILING APPLICATION NUMBER: US/10/187,738
CURRENT FILING DATE: 2022-07-02
PRIOR APPLICATION TEMOVED - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
ENCITH: 93
TYPE: PRT
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P943-0010 NUMBER: US/10/183,014
CURRENT PILLING DATE: 2002-06-26
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SEQ ID NO 244
LENGTH: 93
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Application US/10183014
5. US20030064441A1
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Smith, Victoria
Watanabe, Colin K.
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Watanabe, Colin K.
Wood, William I.
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Godowski, Paul J.
Gurney, Austin L.
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                                                                  APPLICANT: Baker, Kevin P.
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US-10-187-738-244
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US-10-183-014-244
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61 EHLVEGLRKCVNELGPEASEAVKKLLEALSHLV 93

Search completed: June 2, 2004, 20:25:18 Job time: 17.5802 secs

us-09-700-770-7.rai

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CITY: Abbott Park
STATE: IL
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STRANDEDNESS: sir
TOPOLOGY: linear
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US-08-964-725-14
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Sequence 27, Appl
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Sequence 18,
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Sequence 8,
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2: /cgn2 6/ptodata/2/iaa/5B COMB.pep:*
3: /cgn2 6/ptodata/2/iaa/6A COMB.pep:*
4: /cgn2 6/ptodata/2/iaa/6B COMB.pep:*
5: /cgn2 6/ptodata/2/iaa/PCTUS COMB.pep:*
6: /cgn2 6/ptodata/2/iaa/PCTUS COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-964-725-18

US-08-964-725-19

US-08-964-725-19

US-08-914-725-17

US-09-263-810-4

US-09-263-810-4

US-09-215-918-6

US-09-215-918-6

US-09-215-918-6

US-09-114-000C-3434

US-09-263-810-27

US-09-263-810-27

US-09-283-169-27

US-09-283-169-27

US-09-328-352-7140

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US-09-082-253-7

US-09-162-253-7
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US-08-933-149-8
US-09-082-343-8
US-09-082-253-8
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Match Length
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Sequence 1, Appli Sequence 8, Appli Sequence 8, Appli	Sequence 8, Appli Sequence 2, Appli Sequence 5830, Ap		Sequence 16, Appl Sequence 6, Appli	9900	Sequence 22, Appl Sequence 22, Appl	Sequence 3880, Ap Sequence 21, Appl	Sequence 7, Appli Sequence 7, Appli
US-08-987-505-1 US-09-162-622-8 US-09-509-015-8	PCT-US96-08235-8 US-09-647-224A-2 US-09-543-6813-5830	US-09-252-991A-28767 US-09-134-001C-4739	US-08-964-725-16 US-09-646-028-6	US-09-134-000C-6372 US-09-489-039A-9900	US-07-778-413E-22 US-08-340-102-22	US-09-134-000C-3880 US-09-800-170-21	US-07-731-157A-7 US-08-541-780-7
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99 166 166	390	789	13	147 579	76 76	185 527	774
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66.5 66.5 66.5	66.5	2	64 64	63.5	63 63	63	93
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                                                                                                                                                                                                                                                                                                        APPLICANT: FALLED.
APPLICANT: GORDON, Julian
APPLICANT: HODGES, Steven C.
APPLICANT: KLASS, Michael R.
APPLICANT: KRATCCHVIL, Jon D.
APPLICANT: ROBERTS-RAPP, Lisa
APPLICANT: STROUPE, Steven D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
TITLE OF INVENTION: POR DETECTING DISEASES OF THE LUNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TIEE:
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASISEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/964,725
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/964,725
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BECKET, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 35,441
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REFERENCE/DOCKET NUMBER: 35,441
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                                                                                                                                                     US-08-964-725-18
; Sequence 18, Application US/08964725
; Patent No. 5939265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 19
CORRESPONDINGE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
                                                                                                                                                                                                                                                           COHEN, Maurice
FRIEDMAN, Paula N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: No. 5939265e
                           25 NKVPLPVDKLAPLPLD 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 LRKCVNELGPEASEA 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
I.ENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
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                                                                                                                                                                                                            Patent No. 5939265
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
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                                                                                                                                                                                                          , Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 4
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APPLICANT: COHEN, Maurice
APPLICANT: GORDON, Julian
APPLICANT: GORDON, Julian
APPLICANT: HONGES, Steven C.
APPLICANT: RLASS, Michael R.
APPLICANT: ROBERTS-RAPP, Lisa
APPLICANT: ROBERTS-RAPP, Lisa
APPLICANT: RUSSELL, John C.
APPLICANT: STROUPE, Steven D.
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE LUNG
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                100.0%; Score 459; DB 2; Length 93; 100.0%; Pred. No. 2.8e-47; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 18.3%; Score 84; DB 2; Length 17; Best Local Similarity 100.0%; Pred. No. 0.0012; Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/964,725
                                                                                                                                                                                                                                                                                                                                   61 EHLVEGLRKCVNELGPEASEAVKKLLEALSHLV 93
                                                                                                                                                                                                                                                                                               61 EHLVEGLRKCVNELGPEASEAVKKLLEALSHLV 93
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NAME: ATTORNAY AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REPRENCE/POCKET VMBER: 5997.US.P1
TELECOMMUNICATION:
TELEPHONE: 847/935-1729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 15, Application US/08964725
Patent No. 5939265
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Abbott Laboratories
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 100 Abbott Park Road
CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
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           MOLECULE TYPE: No. 5939265e
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                                                                                                                                          93; Conservative
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                     Query Match
Best Local Similarity
Matches 93; Conserv
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                   , MOLECULE TYI
US-08-964-725-14
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Sequence 4, Application US/08821451A
Patent No. 6066724
GENERAL INFORMATION:
APPLICANT: Jian Ni, Guo-Liang Yu and Reiner Gentz
TITLE OF INVENTION: Human Endometrial Specific Steroid-
TITLE OF INVENTION: Binding Factor I, II and III
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEB: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEB: CACCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                     SITE: IL
COUNTRY: USA
ZIP: GOO64-300.
ZIP: GOO64-300.
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
APPLICATION DATA:
APPLICATION NUMBER: US/08/964,725
FILING DATE:
CLASSIFICATION NUMBER: US/08/964,725
PRIOR APPLICATION NUMBER:
FILING DATE:
ATTORNEY: AGENT INFORMATION:
NAME: BECKET, Cheryl L.
REGISTRATION NUMBER: 35,441
REGISTRATION NUMBER: 35,441
TELEPHONE: 847/935-1729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 16.6%; Score 76; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matchés 16; Conservative 0; Mismatches
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MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: 1BM PS/2
COMPUTER: 1BM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/821,451A
TLASSIFICATION 315
SLASSIFICATION 315
FRICOR APPLICATION DATA:
APPLICATION NUMBER: 60/014,724
                      ADDRESSEE: Abbett Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 17: SEQUENCE CHARACTERISTICS:
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; MOLECULE TYPE: No. 5939265e
US-08-964-725-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 17 amino acids TYPE: amino acid
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  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: ROSELAND
STATE: NEW JERSEY
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217, Applica.
No. 593245
AD 193245
RAL INFORMATION:
APPLICANT: FRIEDMAN, Paula N.
APPLICANT: FRIEDMAN, Paula N.
APPLICANT: HODGES, Steven C.
APPLICANT: KLASS, Michael R.
APPLICANT: ROBERTERAPP, Lisa
"".CANT: RUSSELL, John C.
APPLICANT: RUSSELL, John C.
""STROUPE, Steven D.
""TROUPE, Steven D.
""TROUPE, STEVEN D.
""" FOR DETECTING DISEASES OF THE LUNG
APPLICANT: FRIEDMAN, Paula N.
APPLICANT: GORDON, Julian
APPLICANT: HODGES, Steven C.
APPLICANT: KLASS, Michael R.
APPLICANT: KRATOCHVIL, Jon D.
APPLICANT: ROBERTS-RAPP, Lisa
APPLICANT: ROBERTS-RAPP, Lisa
APPLICANT: ROBERTS-RAPP, Lisa
APPLICANT: ROBERTS-RAPP, Lisa
APPLICANT: ROBERTS-RAPP, Lisa
APPLICANT: ROBERTS-RAPP, Lisa
APPLICANT: STROUPE, Steven D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
TITLE OF INVENTION: ROR DETECTING DISEASES OF THE LUNG
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Laboratories
STREET: 100 Abbott Park
STREET: 11D
COUNTRY: USA
ZIP: 60064-3500
COMPUTER: LBM Compatible
OMPUTER: Diskette
COMPUTER: PastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICANTON NUMBER: US/08/964,725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 16.8%; Score 77; DB 2; Length 18; Best Local Similarity 100.0%; Pred. No. 0.0091; Matches 17; Conservative 0; Mismatches 0; Indels
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Patent No. 5939265
GENERAL INFORMATION:
APPLICANT: COHEN, Maurice
APPLICANT: FRIEDMAN, Paula N.
APPLICANT: GORDON, Julian
APPLICANT: HODGES, Steven C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BECKEY, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 5997
TELECHONICATION INFORMATION:
TELECHONE: 847/935-1729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTER.STICS:
IENGTH: 18 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5
US-08-964-725-17
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1 MKLVTIFLLVTISLCSYSATAFLINKVPLPVDKLAPLPLDINILPFM---DPL-KLLLKTL 56
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Pred. No. 0.11;
                                                   Query Match 16.4%; Score 75.5; DB 3; Length 90; Best Local Similarity 27.0%; Pred. No. 0.11; Matches 34; Indels Matches 27; Conservative 18; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Kratochvil, Jon D.
APPLICANT: Roberts-Rapp, Lisa
APPLICANT: Russell, John C.
APPLICANT: Stronge, Steven D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE BREAST
                                                                                                                                                                                                                                                                                                                                        57 GISVEHLVE--GLRKCVNELGPE----ASEAVKKLLEALS 90
                                                                                                                                                                                                                                                                                                                                                                                 | : |:|: | 50 DAPPEAVAAKGUKRCIDQMSLQKRSLIAEVLVKILKKCS 89
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ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUW TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Billing-Medel, Patricia A.
                                                                                                                                                                                                                                                                          1 MKLSVCLLLVTLALCCYQANA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3: Abbott Laboratories
100 Abbott Park Road
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Patent No. 6183952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cohen, Maurice
Colpitts, Tracey L.
Friedman, Paula N.
Gordon, Julian
Granados, Edward N.
Hodges, Srewn C.
Klass, Michael R.
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REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16.4%;
27.0%;
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US-08-512-276-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 90 amino acids
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott La
STREET: 100 Abbott P
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Billing-I
APPLICANT: Cohen, M
APPLICANT: Cohen, M
APPLICANT: Friedman
APPLICANT: Friedman
APPLICANT: Granados
APPLICANT: Hodges, I
APPLICANT: Klass, M
APPLICANT: Kratochv,
APPLICANT: Roberts-I
APPLICANT: ROBERS-I
APPLICANT: ROBERS-I
APPLICANT: ROBERS-I
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US-09-263-810-4
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CORRESPONDENCE ADDRESS: ADDRESSE: CARELLA, BYRNE, BAIN, GILFILLAN, ADDRESSEE: CECCHI, STEMART & OLSTEIN STREET: 6 BECCHI, STEMART & OLSTEIN STREET: 6 BECCHI, STEMAR ROAD CITY: ROSELAND STATE: NEW JERSEY COUNTRY: USA JEARE: ADDRESSEY COUNTRY: USA JEARE: ADDRESSEY COUNTRY: USA
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Best Local Similarity 27.0%; Pred. No. 0.11;
Matches 27; Conservative 18; Mismatches 34; Indels 3
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   FILING DATE: March 21, 1996
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 328800-521 (PF257)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEPA: 201-994-1744
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,810
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FILING DATE:
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ATTORNEY TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO TH
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/821,451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/09263810 Patent No. 6174992 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 90 AMINO ACIDS TYPE: AMINO ACID STRANDEDNESS:
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo Sapiens
US-09-215-818-6
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LENGTH: 90
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                                     1 MKLVTIFLLVTISLCSYSATAFLINKVPLPVDKLAPLPLDNILPFM---DPL-KLLLKTL 56
                                                                              ----EFCPALVSELLDPFFISEPLFKLSLAKF 49
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Gaps
21;
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16.4%; Score 75.5; DB 4; Length 90;
Best Local Similarity 27.0%; Pred. No. 0.11;
Matches 27; Conservative 18; Mismatches 34; Indels
18; Mismatches 34; Indels
                                                                                                                                                                                                                                                                      Sequence 4, Application US/09583169
Patent No. 6338948
GENERAL INFORMATION:
APPLICANT: Jian Ni, Guo-Liang Yu and Reiner Gentz
TITLE OF INVENTION: Human Endometrial Specific Steroid-
TITLE OF INVENTION: Binding Factor I, II and III
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                                                                                                                                                    | : | :: | :: | 50 DAPPEAVAAKLGVKRCTDQMSLQKRSLIABVLVKILKKCS 89
                                                                                                                          57 GISVEHLVE--GLRKCVNELGPE----ASEAVKULEALS 90
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REGISTRATION NUMBER: 33,073
REPERENCE/DOCKET NUMBER: 325800-521 (PF257)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEPHONE: 201-994-1704
TELEPHONE: 201-994-1704
TELEPHONE: 201-994-1710
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/583,169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/821,451
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
                                                                                   1 MKLSVCLLLVTLALCCYOANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
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    27; Conservative
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STATE: NEW JERSEY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: AMINO ACID
STRANDEDNESS:
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ZIP: 07068
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US-09-583-169-4
      Matches
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Sequence 6, Application US/09215818A Patent No. 6379671

US-09-215-818-6

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16.4%; Score 75.5; DB 4; Length 90;
Best Local Similarity 27.0%; Pred. No. 0.11;
Matches 27; Conservative 18; Mismatches 34; Indels
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Best Local Similarity 27.0%; Pred. No. 0.11;
Matches 27; Conservative 18; Mismatches 34; Indels :
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TITLE OF INVENTION: REAGENTS AND METHODS USEFUL FOR
TITLE OF INVENTION: DETECTING DISEASES OF THE BREAST
FILE REPERENCE: 5972.US.P2
CURRENT APPLICATION NUMBER: US/09/215,818A
CURRENT FILING DATE: 1999-12-18
EARLIER APPLICATION NUMBER: 08/912,276
EARLIER APPLICATION NUMBER: 08/691,105
EARLIER APPLICATION NUMBER: 08/697,105
EARLIER PILING DATE: 1997-08-15
EARLIER FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FABSEQ for Windows Version 3.0
SEQ ID NOS 6
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1 MKLVTIFLLVTISLCSY-SATAFLINKVPLPVDKLAPLPLDNILPFMDPLKLLLKTLGIS 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Jian Ni, Guo-Liang Yu and Reiner Gentz
TITLE OF INVENTION: Human Endometrial Specific Steroid-
TITLE OF INVENTION: Binding Factor I, II and III
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLIAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 69; DB 3;
Pred. No. 0.71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.0%; Score 69; DB 3; 27.5%; Pred. No. 0.71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: CARBILA, BYRNE, BAIN, GILFILLAN, E: CECCHI, STEWART & OLSTEIN 6 BECKER FARM ROAD
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REFERENCE/DOCKET NUMBER: 325800-521 (PF257)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 -VEHLVEGLRKCVNELGPEASEAVKKLLEAL 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | : | | : : | : | | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21; Mismatches
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/821,451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 27, Application US/09263810 Patent No. 6174992
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REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 32:
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 201-994-1700
                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.0%;
27.5%;
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SEQUENCE CHARACTERISTICS:
TRUGTH: 95 AMINO ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 27.5%
Matches 25; Conservative
                                                                                                                                   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 95 AMINO ACIDS
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                                                                                                          201-994-1744
                                                                                                                                                                                                                                          TYPE: AMINO ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: ROSELAND
STATE: NEW JERSEY
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Best Local Similarity
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ZIP: 07068
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                                                                            TELEPHONE:
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US-09-134-000C-3434
US-09-134-000C-3434
Sequence 3434, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: LAYD DOUGHTE-Stamm et al
APPLICANT: LAYD DOUGHTE-SCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BUTEROCCCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT PILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR PILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PATENT NOS: 6812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 VTIFLLVIISLC--SYSATAF-LINKV-PLPVDKLAPLPLDNILPFMDPLKLL---LKTL 56
                  ----EFCPALVSELLDFFFISEPLFKLSLAKF 49
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Best Local Similarity 26.3%; Pred. No. 1.8;
Matches 26; Conservative 29; Mismatches 34; Indels
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Patent No. 6066724
GENERAL INFORMATION:
TITLE OF INVENTION: Human Endometrial Specific Steroid-TITLE OF INVENTION: Human Endometrial Specific Steroid-TITLE OF INVENTION: Binding Factor I, II and III
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   368 GVGLQNRLHLDSMIRRFLKEIQQVSSEKSKSLKQLANDL 406
                                                                                                                                50 DAPPEAVAAKLGVKRCTDQMSLQKRSLIAEVLVKILKKCS 89
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                                                                                    57 GISVEHLVE--GLRKCVNELGPE----ASEAVKKLLEALS
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MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: 1BM PS/2
COPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/821,451A
FILING DATE: March 21, 1997
CLASSIFICATION: 435
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APPLICATION NUMBER: 60/014,724
FILING DATE: March 21, 1996
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 33,073
                     1 MKLSVCLLLVTLALCCYQANA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) ORGANISM: Enterococcus faecalis
US-09-134-000C-3434
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ADDRESSEE:
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SEQ ID NO 3434
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1 MKLVTIFLLVTISLCSY-SATAFLINKVPLPVDKLAPLPLDNILPFMDPLKLLLKTLGIS 59
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                                                                                                         8; Gaps
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Sequence 27, Application US/09583169
Sequence 27, Application US/09583169
Sequence 27, Application US/09583169
Sequence 27, Application US/09583169
Sequence 27, Application US/09583169
Septicant US OF UNENTION:
Human Endometrial Specific Steroid TITLE OF INVENTION:
Human Endometrial Specific Steroid TITLE OF INVENTION:
HUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GLIFTILLAN,
ADDRESSEE: CARELLAN, STEWART & CLSTEIN
STREET: RESCHI, STEWART & CLSTEIN
COUNTRY: USA
STREET: NEW JESSEY
COUNTRY: USA
STREET: NEW JESSEY
COMPUTER READABLE FORM:
MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION UNDRER: US/09/583,169
FILING DATE:
CLASSIFICATION UNDRER: US/09/583,169
FILING DATE:
ATTORNEY/AGENT INFORMATION:
TELECAMMULICATION UNDRER: 33,073
REFERENCE/DOCKET NUMBER: 33,073

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Best Local Similarity 27.5%; Pred. No. 0.71;
Matches 25; Conservative 21; Mismatches 37; Indels
21; Mismatches 37; Indels
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       25; Conservative
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          Matches
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Search completed: June 2, 2004, 20:23:15 Job time: 7.48136 secs

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2, 2004, 19:59:24; Search time 22.1572 Seconds (without alignments) 1185.931 Million cell updates/sec
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1 MKLVTIFLLVTISLCSYSAT......LGPEASEAVKKLLEALSHLV 93
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                   OM protein - protein search, using sw model
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geneseqp2003as:*
geneseqp2003bs:*
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Maximum DB seq length: 200000000
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                                                                                                                                       June
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		Description				σ.						Abr65648	Abu99588	~	8	Abr68197	Aa019894	Abu96250	Abu92681	Abo08758	Abo02810	Abr74964	Abr94726	Abu85699	Abu98859	Abu98074	Abu91780
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Sequence 93 AA;

Human Human	Abr59306 Human sec Abo09368 Human sec Abo19232 Novel hum
ABU89473 ABU86314 ABU86314 ABU80555 ABR08663 ABR99473 ABO18927 ABR18348 ABO18927 ABU85084 ABU85084 ABU85084 ABU85084 ABU85084 ABU85084 ABU85084 ABU85084 ABU85084 ABU85084	ABR59306 ABO09368 ABO19232
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ALIGNMENTS

AAW62068 standard; protein; 93 AA.

RESULT 1 **AAW**6206B

The present sequence represents the protein for lung tissue gene LU103. A method has been developed for detecting the presence of a target LU103 polynucleotide in a test sample, comprising: (a) contacting the sample with at least 1 LU103-specific polynucleotide, and (b) detecting the target LU103 polynucleotide in the test sample, where the LU103 polynucleotide has at least 50% identity to the 269, 263, 225, 507 or 519 bp nucleic acid sequence given in AAV38066 to AAV38070. The methods and products of the present invention may be used to detect, diagnose, stage, monitor, prognose, prevent, treat or determine the predisposition diseases and conditions of the lung, e.g. lung cancer Iung tissue derived polynucleotide LV103 - useful to detect, diagnose, stage, monitor, prognose, prevent, treat or determine pre-disposition to lung disease, e.g. lung cancer. Human; lung tissue gene; LU103; detection; lung cancer; diagnosis. Klass MR; Stroupe SD; Hodges SC, Russell JC, Human lung tissue gene LU103 protein. Cohen M, Friedman PN, Gordon J, Kratochvill JD, Roberts-Rapp L, Claim 20; Page 70; 86pp; English. 96US-00744211. 97WO-US020680. N-PSDB; AAV38069, AAV38070. 14-SEP-1998 (first entry) WPI; 1998-286957/25. (ABBO) ABBOTT LAB. WO9820143-A1. Homo sapiens. 15-NOV-1997; 05-NOV-1996; 14-MAY-1998. Cohen M, AAW62068;

93;

Matches

Query Match Best Local

61

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Human; signal peptide-containing protein; HSPP; diagnosis; cancer;
inflammation; cardiovascular disease; anticancer; anti-inflammatory;
antimicrobial; nootropic; neuroprotective; cardiovascular; hepatotropic;
antiasthmatic; gene therapy; cell proliferation; neurological disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKLVTIFLLVTISLCSYSATAFLINKVPLPVDKLAPLPLDUNLDFMDPLKLLLKTLGISV 60
                                                                                                                                                                                                                  Specific Gene; LSG; Lng101; human; diagnostic marker; prognosticate; cancer; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is a lung specific gene (LSG) protein Lng101 from human clone ID 126758. The LSG has high level of tissue specificity for lungs and is overexpressed in cancerous tissues. The sequence serves as diagnostic marker for detecting, monitoring, staging and prognosticating lung cancer. The diagnosis involves comparing levels of LSG in samples obtained from patient and normal control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A rew method for diagnosing, monitoring and staging lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human signal peptide containing protein HSPP-66 SEQ ID NO:66.
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EHLVEGLRKCVNELGPEASEAVKKLLEALSHLV 93
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                                                                                                                                                                                     Human lung specific gene protein Lng101.
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                                                                                      AAY44456 standard; protein; 93
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                             LU103; amino acid; lung cancer; detection; FISH; Fluorescent in situ hybridisation; protein.
                              100.0%; Score 459; DB 2;
100.0%; Pred. No. 5.6e-47;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                               LU103 specific amino acid consensus sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the lung such as lung cancer
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93; Conservative C
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                                                                       Conservative
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                                                     Similarity
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Homo sapiens.

Synthetic.

19-0CT-1999

AAY28334;

RESULT 2 AAY28334

US5939265-A.

17-AUG-1999

05-NOV-1997; 05-NOV-1996; Friedman PN,

Query Match

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Gaps

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AAU29145 standard; protein; 93 AA.

(first entry)

18-DEC-2001

AAU29145;

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RESULT 5
AAU29145
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              cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia; asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia; Parkinson's disease; Huntington's diseases; ovulatory defect;
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H, Patterson C, Reddy R, Hillman JL;
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reproductive disorder; developmental disorder; arteriosclerosis;
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Au-Young J, Yue H,
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98US-0094983P.
98US-0102686P.
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                                                                                muscular dystrophy
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                                                                                                                       Homo sapiens.
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11-DEC-1998;
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PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha; blood; chondrocyte cell; cell proliferation; cell differentiation; colon; adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Godowski PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Goddard A, Go.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wood WI,
                                       Human PRO polypeptide sequence #122.
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Watanabe CK, W
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2000US-0198121P.
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25-APR-2000;
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31-MAR-1998;
31-MAR-1998;
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08-APR-1998;
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07-MAY-1998;
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22-MAY-1998;
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20-MAR-1998;
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11-MAR-1998;
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                                                                                           10-MAR-1998
Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.

The PRO polypeptides and their associated nucleic acids can be used to detect the presence of a tumour in a mammal by comparing the level of expression of a PRO polypeptide in a test sample of cells from the animal and a control sample of normal cells, whereby a higher level of and a control sample of normal cells, whereby a higher level of mammal include dogs, cats, cattle, horses, sheep, pigs, goats and rabbits but are preferably human. The polypeptides can be used to stimulate tumour necrosis factor (TNF) alpha release from human blood, when contacted with it. A specific polypeptide can be used to stimulate the proliferation or differentiation of chondrocyte cells. The PRO proteins can be used to determine the presence of tumours and also susceptibility to tumour development, particularly adrenal, lung, colon, breast, prostate, rectal, cervical, or liver tumours, in mammalian subjects. The oligonucleotide probes specific for the PRO nucleic acids can be used for genetic analysis of individuals with genetic disorders
 presence of tumors, such as prostate and breast tumors, in mammals and to screen for modulators of the compounds.
                                                                                                                                                                                                                                                                                                                                                                               1 MKLVTIFLLVTISLCSYSATAFLINKVPLPVDKLAPLPLDNILPFMDPLKLLLKTLGISV 60
                                                                                                                                                                                                                                                                                                                                                                                                Human, PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver; dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT; antibody-dependent enzyme mediated prodrug therapy.
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                                             Claim 11; Fig 244; 774pp; English
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97US-0062250P.
97US-0063121P.
97US-0063121P.
97US-0063541P.
97US-0063544P.
97US-0063544P.
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24-OCT-1997;
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29-0CT-1997;
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PR 17-JUN-1998; 980C-008952P.
PR 19-JUN-1998; 980C-008952P.
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PR 24-JUN-1998; 980C-009954P.
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PR 18-AUG-1998; 980C-009963P.
PR 18-SEP-1998; 980C-009963P.
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Conservative 0; Mismatches 0;
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                                                                                                                                                                     Similarity
93; Conserv
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12-DEC-1997;
12-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                 tissue typing
                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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      23-SEP-1998;
24-SEP-1998;
24-SEP-1998;
24-SEP-1998;
25-SEP-1998;
29-SEP-1998;
29-SEP-1998;
30-SEP-1998;
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                                                                                                                                                             Query Match
                                                                                                                                                                      Best Local
Matches 9
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98US-0090429P.
98US-0090444P.
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98US-0090444P.
98US-0090646IP.
98US-0090646IP.
98US-0090646P.
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98US-00919P.
98US-00919P.
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98US-0100849P.
98US-010104P.
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98US-0101473P.
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98US-0101738P.
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17-AUG-1998;
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17-AUG-1998;
18-AUG-1998;
18-AUG-1998;
18-AUG-1998;
26-AUG-1999;
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26-AUG-1999;
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18-SEP-1998;
18-SEP-1998;
23-SEP-1998;
23-SEP-1998;
23-SEP-1998;
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17-SEP-1998;
17-SEP-1998;
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01-SEP-1998;
02-SEP-1998;
02-SEP-1998;
02-SEP-1998;
09-SEP-1998;
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10-SEP-1998;
15-SEP-1998;
22-JUN-1998;
24-JUN-1998;
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24-JUN-1998;
25-JUN-1998;
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26-JUN-1998;
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16-SEP-1998;
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25-JUN-1998;
25-JUN-1998;
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01-JUL-1998;
01-JUL-1998;
02-JUL-1998;
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02-JUL-1998;
02-JUL-1998;
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26-AUG-1998;
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                                                                                                                                                                       MKLVTIFLLVTISLCSYSATAFLINKVPLPVDKLAPLPLDNILPFMDPLKLLLKTLGISV
                                                                                                                                                                                   Gaps
                                                                                                                                                       .;
0
                                                                                                                                     6; Length 93;
                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                 Human secreted polypeptide PRO1128, SEQ ID NO:244.
                                                                                                                                    Score 459; DB 6;
Pred. No. 5.6e-47;
                                                                                                                                                                                                             61 EHLVEGLRKCVNELGPEASEAVKKLLEALSHLV 93
                                                                                                                                                       0; Mismatches
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                                                                                                                                                                                                                                                                              ABR66258 standard; protein; 93 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97US-0059263P.
97US-0062250P.
97US-0062250P.
97US-0063120P.
97US-0063121P.
97US-0063541P.
97US-0063544P.
97US-006354P.
97US-006354P.
97US-006354P.
97US-006354P.
97US-006351P.
97US-0064120P.
97US-006646EP.
97US-006646EP.
       980S-0102207P
980S-010230P
980S-0102331P
980S-0102331P
980S-0102570P
980S-0102571P
980S-0102684P
980S-0102687P
980S-0102687P
980S-0102687P
980S-0102687P
                                                                                                                                      100.0%;
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98US-0101786P
                                                                                                                                                                                                                                                                                                                  05-AUG-2003 (first entry)
                                                                                                                                               Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  US2003027278-A1.
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24-OCT-1997;
24-OCT-1997;
28-OCT-1997;
28-OCT-1997;
28-OCT-1997;
31-OCT-1997;
31-OCT-1997;
31-OCT-1997;
31-OCT-1997;
29-OCT-1997;
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12-DEC-1997
25-SEP-1998,
29-SEP-1998,
29-SEP-1998,
29-SEP-1998,
30-SEP-1998,
30-SEP-1998,
30-SEP-1998,
01-OCT-1998,
06-OCT-1998,
06-OCT-1998,
07-OCT-1998,
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                                                                                                                                        Query Match
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18-0069870P 18-0068017P 18-0077450P 18-0077632P 18-0078886P 18-0078886P 18-0078886P 18-007864P 18-0080134P 18-0080137P	98 98 98 98 98 98 98 98 98 98 98 98 98 9	US-00876091 US-00877591 US-00887251 US-00880281 US-00880281 US-00881256 US-00881256 US-00881257 US-00881257 US-00881257 US-00881257 US-0088738 US-0088738 US-0088738 US-0088738 US-0088738 US-0088738 US-0088738 US-0088738 US-0088738 US-0088738 US-0088738 US-0088738 US-0088738 US-0088738	JUS-00891US 3US-008951Z 3US-0089538 8US-0089598 8US-0089598 8US-0089908 8US-0089908
DEC-1997 MAR-1998 MAR-1998 MAR-1998 MAR-1998 MAR-1998 MAR-1998 MAR-1998 MAR-1998 MAR-1998	08-APR-1998; 08-APR-1998; 15-APR-1998; 21-APR-1998; 22-APR-1998; 22-APR-1998; 22-APR-1998; 29-APR-1998; 29-APR-1998; 29-APR-1998; 29-APR-1998; 07-MAY-1998; 07-MAY-1998; 07-MAY-1998; 07-MAY-1998; 15-MAY-1998; 15-MAY-1998; 15-MAY-1998; 15-MAY-1998; 15-MAY-1998; 15-MAY-1998; 22-MAY-1998; 22-MAY-1998; 22-MAY-1998; 22-MAY-1998; 22-MAY-1998; 22-MAY-1998; 28-MAY-1998;	2008-1999 2008-1999	2-70N-199 5-70N-199 7-70N-199 7-70N-199 8-70N-199 8-70N-199 8-70N-199
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98US-0090254P.
98US-0090435P.
98US-0090444P.
98US-0090444P.
98US-0090444P.
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9805-0088212P

9805-0088212P

9805-008872P

9805-0088740P

9805-0088740P

9805-008825P

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9805-0088039P.
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22-JUN-1998;
24-JUN-1998;
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22-APR-1998;
22-APR-1998;
28-APR-1998;
29-APR-1998;
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05-MAX-1998

07-MAX-1998

07-MAX-1998

07-MAX-1998

15-MAX-1998

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15-MAX-1998

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22-MAX-1998

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28-MAX-1998
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                                                                                   01-APR-1998;
08-APR-1998;
08-APR-1998;
09-APR-1998;
15-APR-1998;
21-APR-1998;
        11-MAR-1998;
20-MAR-1998;
20-MAR-1998;
27-MAR-1998;
31-MAR-1998;
31-MAR-1998;
01-APR-1998;
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                                                                                                                                                                       Gaps
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                                                                                                                              5.6e-47;
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                                                                                                                     Score 459; DB Fred. No. 5.6e-0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97US-0059266P.
97US-0059266P.
97US-0063486P.
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97US-006311P.
97US-006371P.
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97US-006371P.
97US-006371P.
97US-006412P.
97US-006412P.
97US-006412P.
97US-006412P.
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  98US-0101922P.
98US-0101786P.
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98US-0102310P.
98US-0102311P.
98US-0102311P.
98US-0102570P.
98US-0102571P.
98US-0102571P.
                                                                                                                       100.0%;
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                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 93; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-JUL-2002;
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28-0CT-1997;
28-0CT-1997;
28-0CT-1997;
28-0CT-1997;
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31-OCT-1997;
31-OCT-1997;
13-NOV-1997;
21-NOV-1997;
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  24.5EP-1998;
25.5EP-1998;
29.5EP-1998;
29.5EP-1998;
29.5EP-1998;
30.5EP-1998;
30.5EP-1998;
30.5EP-1998;
30.5EP-1998;
30.5EP-1998;
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10-MAR-1998;
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17-OCT-1997;
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17-DEC-1997
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24-OCT-1997
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ABR65648
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PR 24-7UN-1998; 98108-0109445P.

PR 24-7UN-1998; 98108-0109644P.

PR 24-7UN-1998; 98108-0109644P.

PR 24-7UN-1998; 98108-0109644P.

PR 24-7UN-1998; 98108-0109648P.

PR 25-7UN-1998; 98108-010965P.

PR 25-7UN-1998; 98108-010969P.

PR 25-7UN-1998; 98108-010
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                                                                                                                    MKLVTIFLLVTISLCSYSATAFLINKVPLPVDKLAPLPLDNILPFMDPLKLLLKTLGISV
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                                                                                                                                                                                                                                                                                             Human; secreted and transmembrane protein; PRO; INF-alpha;
tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
tissue typing.
                                                                                                   Gaps
                                                                                                   .;
0
                                                                                Length 93;
                                                                                                   Indels
                                                                                100.0%; Score 459; DB 6;
ilarity 100.0%; Pred. No. 5.6e-47;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                               Human secreted/transmembrane protein (PRO) #122.
                                                                                                                                                         93
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97US-0063486P.
97US-006312DP.
97US-0063121P.
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97US-007987P.
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980S-0102331P.
980S-0102487P.
980S-0102571P.
980S-0102571P.
980S-0102684P.
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98US-0102240P
                                                                                                                                                                                                                                                               09-F.UG-2003 (first entry)
                                                                                            Similarity
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20-MAR-1998;
27-MAR-1998;
27-MAR-1998;
31-MAR-1998;
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24-0CT-1997;
24-0CT-1997;
28-0CT-1997;
28-0CT-1997;
28-0CT-1997;
29-0CT-1997;
21-0CT-1997;
21-0CT-1997;
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21-0CT-1997;
24-0CT-1997;
24-0CT-1997;
24-0CT-1997;
24-0CT-1997;
24-0CT-1997;
24-0CT-1997;
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10-MAR-1998;
11-MAR-1998;
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12-DEC-1997;
17-DEC-1997;
29-SEP-1998;
29-SEP-1998;
30-SEP-1998;
30-SEP-1998;
30-SEP-1998;
01-OCT-1998;
01-OCT-1998;
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                                                                                  Query Match
Best Local Simil
Matches 93; C
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Matches 93; Conservative
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The present invention provides the human and murine uteroglobin related protein 1 (UGRP1) promoters. The sequences can be used in the diagnosis of and prediction of predisposition to respiratory disorders such as asthma. The present sequence is a protein sequence shown in the exemplification of the invention
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             MKLVTI FLLVTI SLCSYSATAFLINKVPLPVDKLAPLPLDNILPFMDPLKLLLKTLGISV
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                                                                                                                                                                                                                                                                                                                                                                                       Human uteroglobin related protein 1.
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                                                                                                                                                                                                                                                          AAO:19894 standard; protein; 93 AA
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